F;2202-2209/Region: nucleotide-binding motif A (P-loop) F;2530-2537/Region: nucleotide-binding motif A (P-loop)

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Accession: B60950

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C;Species: Halobacterrium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Letthauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jable, Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Anuthors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig. 22 [imported] - Arabidopsis thaliana (cipes)
Cipecies: Arabidopsis thaliana (mouse-ear cress)
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cipate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, C.; Alonso, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Lin, X.; Liu, Z.A.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rewley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719; PMID:11130712
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39801
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, July 1999
A;Recession: T39801
A;Accession: T39801
A;Accession: T39801
A;Accession: T39801
A;Accession: Deliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DDA
A;Residues: 1-501 cMCD>
A;Cross-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBC19C2.10
A;Experimental source: strain 972h-; cosmid c19C2
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A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
C;Genetics:
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hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
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llarity 41.7%; Pred. No. 56;
Conservative 3; Mismatches 4; Indels
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Pred. No. 48;
1; Mismatches
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
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A;Introns: 196/3
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A,Residues: 1-274 < LAM>
A,Note: authors translated the codon ATA for residue 8 as Val
C,Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'vauinors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome; Reference number: A70500; MUID:98295987; PMID:9634230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70655
C;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
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A.; Lipid Res. 31, 1109-1120, 1990
A.; Tile: A cross-species comparison of the apolipoprotein B domain that binds to the 1 A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Recession: B60950
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
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                                                                                                                         Ouery Match 56.7%; Score 38; DB 2; Length 4568; Best Local Similarity 41.7%; Pred. No. 2.7e+02; Matches 5; Conservative 3; Mismatches 4; Indels
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Best Local Similarity Matches 6; Consery 4 WXRNMRKVR 12 39 WDRNLRKFR 47

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Query Match

hypothetical sh3-containing protein C; Species: Schizosaccharomyces pombe

RESULT 12 T39801

Conservative

Best Local Similarity Matches 6; Conserv

A; Gene: Rv3854c

Genetics:

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Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
Accession: AD2346
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.;Status: preliminary
.;Molecule type: DNA
.;Residues: 1-124 <STO>
.;Cross-references: GB:AE005173; NID:94587555; PIDN:AAD25786.1; GSPDB:GN00141
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,Gene: F1511.22
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SEQUENCE OF 237-711 FROM N.A.

MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Mhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastida M., Kaplan N., Greco T., Touchman J., Muzny D.,

Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,

Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

Sagripanti J.L.,

Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
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MEDLINE=82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.N.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz B.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an expression of mRNA during normal and leukemic myelopoiesis.";
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MEDLINE=85076667; PubMed=6510420;
MELZ-Boutique M.-H., Jolles J., Maurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";

Eur. J. Blochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
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Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at
"seolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jolles P.; "An 88 amino acid long C-terminal sequence of human
                                                                                       Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N- and C-terminal domains.";
Biochim. Biophys, Acta 670:243-254(1981).
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MEDLINE=99190892; PubMed=10089347;
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                                   TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
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Biochemistry 36:341-346(1997).
[17]
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SEQUENCE OF 3-711 FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its worfite by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
A. Gugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
B. Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
Teamilial subspithelial corneal amyloidosis (gelatinous drop-like
orneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998).
Corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998).
CORN BINDING TRANSPORT PROTEINS WHICH
CORN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICKBOMATE.
CORN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICKBOMATE.
CORN BINDING TRANSPORT PROTEINS, WHILE
CORN CORPERROXIN B AND C HAVE OFFICEPRORS, WHILE
CLACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                        MEDINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                   MEDLINE=99192677; PubMed=10089508; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: MONOMER.
-: SUBCELLULAR LOCATION: Secreted.
-!- DOWAIN: COMPOSED OF TWO HOWOLOGOUS DOWAINS.
-!- DOWAIN: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                   Agric. Biol. Chem. 54:1803-1810(1990).
                                                          Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                         CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X53961, CAA37914.1, EMBL, U07643, AAB60324.1; EMBL, M93150, AAA36159.1; EMBL, M83202, AAA59511.1, EMBL, M83205, AAA58656.1; EMBL, M83205, AAA6665.1; EMBL, AF332168, AA46665.1; EMBL, BC015822, AAH15822.1; EMBL, BC015823, AAH15822.1; EMBL, X52941; CAA37116.1, EMBL, X52941; CAA37116.1; EMBL, V95626, AAB57795.1; -
                                                                                                                                                                                                                                                                                                                                                                         VARIANTS THR-30 AND ARG-48.
PubMed=9873069;
                                                                                                                                                                                                                                                                                                                     from human lactoferrin."
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1LFG; 31-JUL-94.
1LFH; 31-OCT-93.
1LFI; 31-OCT-93.
1LGB; 31-AUG-94.
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08-MAR-96. 12-MAR-97.

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TRFL CAPHI STANDARD; PRT; 708 AA. Q29477; Q29477; Q29479; STANDARD; STANDARD; DESTRUCTORS (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                     71.6%; Score 48; DB 1, 66.7%; Pred. No. 0.21;
BY SIMILARITY.
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es 8; Conserv
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Submitted (UNI-1995) to the EMBL/GenBank/DDBA databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
-CAN BIND TWO NSTALLY BICARBONATE (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCINIT: MONOMER (BY SIMILARITY).
-!- SUBCILILLAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                      Gaps
                                                                                                                                                                                                                                            Camelus dromedarius (Dromedary) (Arabian camel).

Bukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Tylopoda; Camelidae, Camelus,
                                                                                                                                                                                                                                                                                                                          STRAIN-Somali, TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, 077811, 1BX.
InterPro; IPR001156; Transferrin.
Pfam; PF00402; transferrin; 2.
PRINTS; PR00402; TRANSFERRIN; 3.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN]; 2.
PROSITE; PS00206; TRANSFERRIN]; 2.
PROSITE; PS00207; TRANSFERRIN]; 2.
PROSITE; PS00207; TRANSFERRIN]; 2.
PROSITE; PS00207; TRANSFERRIN]; 2.
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             Length 711;
            Score 65; DB 1; Length 711
Pred. No. 0.00015;
0; Mismatches 1; Indels
                                                                                                                                                             BY SIMILARITY.
LACTOTRANSFERRIN
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         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                      STANDARD;
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Capra hircus (Goat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butharia; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                                                                                                                                                                                                                       (POTENTIAL).
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(POTENTIAL).
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304 G -> A (IN REF. 2).
494 LLS -> PLF (IN REF. 2).
506 L -> F (IN REF. 2).
609 A -> P (IN REF. 2).
613 A -> P (IN REF. 2).
77211 MW, 080C175A0B69D430 CRC64;
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
BY SIMILARITY.

BY SIMILARITY.

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 1 (BY SIMILARITY).

IRON 2 (BY SIMILARITY).

IRON 3 (BY SIMILARITY).

ANION (BY SIMILARITY).

N-LINKED (GLCNAC...)

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MILA DROME STANDARD; PRT; 292 AA.

09XZL8; 09V391;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2010 (Rel. 39, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Nebula protein.
NEADLA protein.
Drosophila melanogaster (Fruit fly).
Drosophila melanogaster (Fruit fly).
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.
Nuscomorpha; Ephydroidea; Drosophila.
NCBI_TAXID=7227;
                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IRRO1156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINITS; PR00405; TRANSFERRIN.
SMART; SM0049; TR FER, 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
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LACTOTRANSFERRIN
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EMBL; X78902; CAA55517.1; -.
HSSP; O77698; ICE2.
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RAMEDINE-20196006, PubbMed=10731112;

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RADARR M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADARR M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADARR M.D. Celniker S.E., Holt R.A., Anbburner M., Henderson S.N.,

Sutton G.G., Mortnam J.R., Yandell M.D., Zhang O., Chent L.K.,

RADARR M.R., Boyle C., Baxter E.G., Helt G., Nelson C.R., Malkloo G.L.G.,

RADARIL J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RADARR M., Benos P.V., Berman B.P., Bhandari D., Botalakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RADORON K., Doug L.E., Downes M., Dugan-Rochas S., Pottier P.,

RADORON K.J., Doug L.E., Downes M., Dugan-Rochas S., Pleischmann W.,

RADARR M., Evangellsta C.C., Ferraz C., Ferriera S., Pleischmann W.,

RADARR M., Gabriellan A.E., Garrell J.H., G. Z., Galbart W.M., Glasser K.,

RADARR M., Gabriellan A.E., Garrell J.H., G. Z., Galbart W.M., Glasser K.,

RADARR M., Gabriellan A.E., Garrell J.H., G. Z., Galbart W.M., Glasser K.,

RADARR M., Gabriellan A.E., Garrell J.H., G. Z., Galbart W.M., Glasser K.,

RADARR M., Maryor D., Heiman T.J., Hernandez J.R., Houck J.,

RADARR M., Moylw, W., Worlyn B., Murphy L., Marny D.M., Nelson D.L.,

RADARR M., Moylw, M., Murphy E., Marny D.M., Nelson D.L.,

RADARR M., Moylw, M., Murphy E., Marny D.M., Smith T.,

RADARR M., Moylw, M., Murphy B., Murphy L., Marny D.M., Smith T.,

RADARR M., Moylw, M., Murphy B., Murphy L., Marny D.M., Smith T.,

RADARR M., Moylw, M., Wolley K.C., Wu D., Yang S., Yao Q., Zhen J.,

RADARR M., Zhodh P., Samanna D.J., Wang S., Dollard J., Wang S., Yao Q., Zhan J.,

RADARR M., Zhodh P., Wassaman D.J., Weissenbach J.,

RADARR M., Zhodh P.M., Warny D.M., Strong R., Smith H.O.,

RADARR M., Zhodh P.M., Warny D.M., Strong R., Smith H.O.,

RADARR M., Zhodh P.M., Warny D.M., Wang Senbach J., Wang S., Yao Q., Zhan J., Zhong Y., Wassaman D.A., Weilsen R., Wongay S., Zhong Y
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SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
                                                                                                                                                                                        Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Berkeley;
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Gaps

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Conservative

Best Local Similarity Matches 7; Conserv

1 CFOWXRNMRKV 11 CYQWQRRMRKL 48

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LACTOTRANSFERRIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Uterus;
MEDLINE-87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                :ISSUE=Uterus;
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SEQUENCE
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                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resolution.";
J. Mol. Biol. 289:303-317(1999).

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                        Eŭkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTIE; PS00205; TRANSFERRIN 1; 2.
PROSTIE; PS00206; TRANSFERRIN 1; 2.
PROSTIE; PS002007; TRANSFERRIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
Signal; 3D-structure.
                                                                                                                                     ö
                                                                                                    Query Match
Best Local Similarity 54.5%; Pred. No. 2.6;
Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;

"CDNA sequence of mare lactoferrin.";

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                           EMBL, AF147700, AAD33987.1; -.
EMBL, AB003712; AAF5288.1; -.
FYBRS: FSG0026629; nla.
SEQUENCE 292 AA, 31423 MW, 64F1BBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment)
                                                                                                                                                                                                                                                                       695 AA
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                       PRT;
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InterPro; IPR001156; Transferrin.
Edm; PP00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AJ010930; CAA09407.1; -. PDB; 1B1X; 02-DEC-98. PDB; 1B7U; 02-FEB-99.
                                                                                                                                                                                                                                                                       STANDARD;
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150 FQWLRSFRRLR 160
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"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
0.7BB84D50E1165D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRFL_MOUSE STANDARD; PRT; 707 AA. P08071; P70650; Q61799; Q922P2; C1-AUG-1988 (Rel. 08, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                SEQUENCE OF 1-14 FROM N.A.

MEDLINE=9204209; PubMed=1939212;

Liu Y., Teriz C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991)

-: FONCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03298; AAA40525.1; -.

R EMBL; D88510; BAA13633.1; -.

R EMBL; MA4778; AAA34927.1; -.

R PIR; A28438; A28438.

R HSSP, P02788; 1LE.

R InterPro; IPR001156; Transferrin.

R PRINTS; PR00422; TRANSFERRIN.

R PRINTS; PR00405; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN 1; 1.

R PROSITE; PS00206; TRANSFERRIN 2; 2.

R PROSITE; PS00206; TRANSFERRIN 3; 2.

R PROSITE; PS00207; TRANSFERRIN 3; 2.

R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
ANION (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
R-> 100 (IN REF. 1).
R-> 0 (IN REF. 2).
   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                              -!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOWAINS.
-!- DOMAIN: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
LACTOTRANSFERRIN.
1.
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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

-i- FUNCTION: DNA THO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Planet P., dagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-rpoBC operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RNA)(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1 BETA. CHAIN.
-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-NOV-1995 (Rel. 40, Last annotation update)
101-OCT-2001 (Rel. 40, Last annotation update)
1010-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liberibacter africanus (Liberobacter africanum).
Liberibacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
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                                                                                                                                                                                                        Score 39; DB 1; Length 707;
Pred. No. 9.6;
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InterPro; IPR001572; RNA_pol_B.
PFAM; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
NON_TER 146 146
SEQÜENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
            M -> L (IN REF. 2).
S -> T (IN REF. 2).
A -> D (IN REF. 1).
E -> G (IN REF. 1).
L -> V (IN REF. 1).
W, F26AE0340A4C19A8 CRC64;
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                                                                                                                                                                                                                                                                 1; Mismatches
82
359
382
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77865 MW; F
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Similarity 54.5%;
6; Conservative
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es 6; Conserv
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SEQUENCE FROM N.A.
STRAIN=Nelspruit;
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Best Local Similarity
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SEQUENCE FROM N.A. (A*3401/A*3402).
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DYNEIN HAS ATPASE ACTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
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                                                                                                       Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBL_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 39, Last annotation update)
Dynein dain, flagellar outer arm.
ODA OR ODA OR NPI.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.7%; Score 38; DB 1; Length 783; 50.0%; Pred. No. 16; 1. Indels ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, Z35602; CAMOTO, L., WORMPEP, R13G10.2; CE25088.
InterPro; IPR002337; Amino_oxidase.
Ffan, PF01593, Amino_oxidase, 1.
Hypothetical protein, Oxidoreductase; Flavoprotein; FAD. NP_BIND 311 366 FAD (ADP PART) (POTENTIAL).
                                                                                                                                                                                                                                                                                                 Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                      Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                      TNR2_CAEEL STANDARD; PRT; 783 AA.
021968 (Rel. 37, Created)
15-DBC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last amnotation update)
Hypothetical protein R13G10.2 in chromosome III.
313G10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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540 CIDWGRDDRKVK 551
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                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
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C Q39565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (A*3401/A*3402).
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martiel A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martiell R., W., du Toit E.D., Parham P.,
"Distinctive HiA-A, B antigens of black populations formed by
interallelic conversion.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93235211; PubMed-8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
   (ALPHA, BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1A34 HUMAN STANDARD; PRT; 365 AA.
P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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InterPro; IPR04273; Dynein heavy.
Pfan; PF03028; Dynein heavy; 1.
Motor proțein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 4568;
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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Pred. No. 95;
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Myxoma virus (strain Lausanne).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
     01-OCT-1989 (Rel. 12, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Serine proteinase inhibitor 1 (Serpin 1) (Serp-1)
SERPI OR M008.1L.
                                                                  Leporipoxvirus.
NCBI_TaxID=31530;
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                                                                                                                                                                                                                                                                                                        HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-34 (A-10) ALPHA CHAIN.
EXTRACELIULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
I -> V (IN A*3402).
                                         MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
(AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
      Tissue Antigens 41:72-80(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                       Score 36; DB 1; Length 365; Pred. No. 18; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           I - V (IN A*3402).
/FTId=VAR 004379.
/FTId=VAR 004380.
R - N (IN A*3402).
/FTId=VAR 004381.
P - S (IN A*3402).
/FTId=VAR 004382.
/FTId=VAR 004383.
/FTId=VAR 004383.
W - L (IN A*3402).
/FTId=VAR 004383.
W - L (IN A*3402).
/FTId=VAR 004383.
L - I (IN A*3402).
L - N I (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
                                                                                                                                                             EMBL, X61704, CAA43873.1, -.
EMBL, X61705, CAA43874.1; -.
PIR, S16767, S16767.
PIR, S16771, S16771.
HSSP, O19673, 1HSB.
MIM, 142800, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41055 MW;
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66.7%;
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                                                                     A*3401.
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DOMAIN
TRANSMEM
DOMAIN
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=91049428; PubMed=2173255;
Upton C., Macen J.L., Wishart D.S., McFadden G.;
Upton C., Macen J.L., Wishart abbit fibroma virus encode a serpin-like
"Myxoma virus and malignant rabbit fibroma virus encode a serpin-like
protein important for virus virulence.";
virology 179:618-631(1990).
                                                                                                                                                                                                                                                                                                                                                                         repeats of Shope
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MEDILINE-20032073; PubMed=10562494;
Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
Cameron C., Hota-Mitchell S., Chen L., McPadden G.;
Macaulay C., Willer D., Evans D., McPadden G.;
"The complete DNA sequence of myxoma virus.";
Virology 264:299-318(1999).
-!- FUNCTION: IMPORTANT IN VIRULENCE.
-!- FUNCTION: MAS ORIGINALLY (REF. 2 AND REF. 3) THOUGHT TO ORIGINATE
-!- CAUTION: A PLASMID RABBIT DNA. THE ORIGINAL SAMPLE WAS CONTAMINATED
AND THE GENE IS DERIVED FROM MYXOMA VIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESQUENCE FROM N.A.

BEQUENCE FROM N.A.

MEDLINE=87030884; PubMed=3021526;

Whon C., Carrell R.W., McFadden G.;

"A novel member of the serpin superfamily is encoded on a circular plasmid-like DNA species isolated from rabbit cells.";

FEBS Lett. 207:115-120(1986).
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3 319 320 REACTIVE BOND (BY SIMILARITY).
1 16 MKYLVLVLCLTSCACR -> MFNVVRV (IN
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=87064296; PubMed=3023828;
Upton C., McFadden G.;
"DNA sequence homology between the terminal inverted repeat "DNA sequence homology between sellular plasmid species.";
fibroma virus and an endogenous cellular plasmid species.";
Mol. Cell. Biol. 6:265-276(1986).
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Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels
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8DB31CE131C218A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M35233; AAA46629.1; -.
EMBL; M12333; AAA81567.1; -.
EMBL; AF170726; AAF15055.1; -.
EMBL; AF170726; AAF14896.1; -.
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PIR; B36418; B36418; B36418; B36418; B36418; B36418; B36418; B6721; B7600215; Serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
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InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
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Best Local Similarity 50.0°
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749 AA;
                                                                                                                                      Viruses; dsRNA vi.
NCBI_TaxID=12705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coat protein;
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RL28 THETN
ID RL28 THETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-MOPH / Nigg.
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Bisen J., Fraser C.M.,
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pneumoniae AR39.",

Nucleic Acids Res. 28:1397-1406(2000).

-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidyl-tRNA(His).

-!- SUBUNIT: HOWDIMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: Cytoplasmic.

-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                   i6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (BC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                            Chlamydia muridarum.
Bacteria, Chlamydiales, Chlamydiaceae, Chlamydia.
                                                                                                                                                                                      428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%; Pred. No. 21; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001106; AAtRNA_ligaseII.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004516; HisS-
InterPro; IPR004516; HisS-
InterPro; IPR005314; tRNA-synt_2b.
Pfam; PF00387; tRNA-synt_2b; I.
Pfam; PF03129; HGTP_anticodon; I.
IIGRPAMS; IIGR00442; HisS; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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P4_ROTGA STANDARD;
D VP4_ROTGA STANDARD;
C Q04916;
T 01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002349; AAF39630.1; -.
HSSP; 032422; 1QE0.
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                                                                                                                                                                                   STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome SEQUENCE 428 AA
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                                                  235 WIRNWRK 241
4 WXRNMRK 10
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                                                                                                                                                                                                                                                                                                                                             (HisRS).
HISS OR TC0830
                                                                                                                                                                                   SYH CHLMU
Q9PJJ9;
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Matches

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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDINE-2933240; PubMed-8386274; MEDINE-9333240; PubMed-8386274; MacKow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
MEDLINE=21992816; PubMed=11997336;
MEDLINE=21992816; PubMed=11997336;
Chen Y., Xue Y., Xu Y., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 12:689-700(2002).
-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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(POTENTIAL)
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                            Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                      human group B rotavirus ADRV.";
-/- Virol. 67:2730-2738(193).
-!- SUBCELLUJAR LOCATION: Onter capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; DB 1; Length 749;
Pred. No. 36;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (PC
N-LINKED (GLCNAC. . .) (PC
D1223527DEAE0F21 CRC64;
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(GLCNAC.
(GLCNAC.
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15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92074218; PubMed=1962437;
MEDLINE=92074218; PubMed=1962437;
Dzianott A.M., Bujarski J.J.;
Dzianott A.M., Bujarski J.J.;
Mither nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic mottle virus.";
Virology 185:553-562(1991).
- - FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0TJ-1993 (Rel. 26, Created)
01-0TJ-1993 (Rel. 26, Last sequence update)
01-0TJ-1993 (Rel. 26, Last annotation update)
1A protein [Includes Helicase; Methyltransferase].
Broad bean mottle virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                          Score 35; DB 1; Length 62;
Pred, No. 4.6;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A41699; PIBVBB.
InterPro; IPR005288; Vmethyltransf.
InterPro; IPR000506; Viral helicasel.
Pfam; PF01443; Viral helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
Helicase; ATP-binding; Transferase; Methyltransferase.
NP BIND
SEQUENCE 966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                                   Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
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                                                                                                                                                                                                                                                               52.2%;
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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27 RWKPNIRKVR 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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NCBI_TaxID=12301;
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VIA_BBMV
8246666666666
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1 CFQ----WXRNMRKV 11

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347 CFKENKDWTENMRSV 361
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Search completed: February 21, 2003, 07:51:36 Job time : 6.2093 secs

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Q8xse2 ralscoria s
Q9d73 yaba monkey
Q9daj3 mus musculu
Q9daj3 mus musculu
Q9dy11 mus musculu
Q9dy11 mus musculu
Q9dy5 lumpy skin
Q9dy5 lumpy skin
Q9dy6 yaba-like d
Q9md0 schizoaacch
Q9m3 halobacteri
Q9y34 drosophila
Q9y4c1 human immun
Q9yqc1 human immun
Q9yqc0 human immun
Q9yqb human immun
Q9yjb nuan immun
Q9yjb arabidopsis
Q9nus Apomo sapien
Q9nus Apomo sapien
Q9nus Callicephu
Q9nus Callicephu
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Q9d4x5 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OGUCYS;
10. MAY-2000 (TrEMBLrel. 13, Created)
10. MAY-2000 (TrEMBLrel. 13, Last sequence update)
10. JUN-2001 (TrEMBLrel. 17, Last annotation update)
10. JUN-2001 (TrEMBLrel. 17, Last annotation update)
10. JUN-2001 (Human)
10. Machagens (Traniata, Vertebrata, Euteleostomi)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC02241, AAH2247, 1, - SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     711 AA
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                                                                                                                               Q9HPA3
Q9V346
Q9XFD5
Q9YCC1
Q9YQE9
Q9YQE9
Q9YJI7
Q9YJI7
Q9YJI7
                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                    Q8XSE2
Q9QB73
Q9DAJ3
Q9D9X0
                                                             09JIT1
091MQ5
09DHK5
P96223
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Q8S487
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=PROSTATE;
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oldsymbol{\omega}
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Q9UCY5
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Q8TCD2
셤
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Q9u4m9 leishmania
Q9fhiya arabidopsis
Q8r55 erx2 conver
O81653 hemerocalli
Q9sic0 arabidopsis
Q77855 human immun
Q77856 human immun
Q9787 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q82462 salmonella
Q9xhpl sesamum ind
O31090 rhizobium l
Q93780 caenorhabdi
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Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                       February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Q9UCY5
Q9TR80
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Q9Z462
Q9X1090
Q93780
Q93780
Q9U4M9
Q9U4M9
Q9U4M9
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098100
077855
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sp_lungn:*
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sp_mammal:*
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sp_organelle:*
sp_bage:*
sp_rodent:*
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
sp_archeap:*
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Sp_bacteria:*
Sp_fungi:*
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67
1 CFQWXRNMRKVR 12
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length: 2000000000
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Match Length DB
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Perfect score:
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Result

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Bentley S.D., Holden M.T.G., Sebaihia M.
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Best Local Similarity
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hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWXRNMRKVR
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031090
1D 03108
AC 03109
DT 01-07
DT 01-07
DE HYPOR
OS BACKE
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MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P00788; 1BKA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprine, Ovis.
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Salmonella.
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     Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
NCBL_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                      83.6%; Score 56; DB 4; Length 38; 90.9%; Pred. No. 0.00085; rive 0; Mismatches 1; Indels
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MEDLINE=95127729; PubMed=7827104;
MEDLINE=95127729; PubMed=7827104;
Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; 077698; 1CE2.
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SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                             Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 AA
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                                                                                 SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Local 6, Conserve
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                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Q9TRB0;
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SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
MININES.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Feltwell T., Hamin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Whitehead S., Barrell B.G.; enception and sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
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01-07AN-1998 (TrEMBirel. 05, Last sequence update)
01-07AN-1998 (TrEMBirel. 18, Last sequence update)
01-0CT-2001 (TrEMBirel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                            Nature 413:848-852(2001).
EMBL, AL627276, CAD06049.1, -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Agric. Food Chem. 47:4932,4938(1999).

EMBL; AF091841; AAD42943.1; -.

InterPro; IRR003612; AAI.

InterPro; IRR001768; Try/amyl inhbtr.

PRIM; PF00234; try/alpha_amyl; 1.

PRIMTS; PR00499; AAI.

SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.2%; Score 41; DB 16;
58.3%; Pred. No. 9.9;
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Sesamum indicum (Oriental sesame) (Gingelly)
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1; Mismatches
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                             STRAIN=129XI/SVJ;
MBDLNRB=21676859; PubMed=11802169;
Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
"Multiple new and isolated families within the mouse superfamily of
VIr vomeronasal receptors.";
Nat. Neurosci. 5:134-140(2002).
EMBL; AY065506; AAL47911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania major.
Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Leishmania major chromosome 5 complete sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163772; AAF14642.1;
InterPro. 1 PR003409; MORN.
FPGM.; PF02493; MORN. 4
SEQUENCE 415 AA, 46701 MW; 3E3AD710BF23691E CRC64;
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Pred. No. 20;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 5, Pl clone:MFC19.
Arabidopsis thaliana (Mouse-ear cress).
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Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                         NCBI_TaxID=10090;
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01-MAY-2000
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Q9U4M9;
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Q9FHI9
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Q9U4M9
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                  "Structural and functional organization of the exopolysaccharide biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39."; Mol. Biol. (Mosk) 32:797-804 (1998). BMBL; AF028810; AA88891.1; -. Hypothetical protein. SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
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                                                                                                                                                                                    Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
Ksenzenko V.N.;
                                                                       Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      59.7%; Score 40; DB 2; Length 273; 60.0%; Pred. No. 8.1; ive 3; Mismatches 1; Indels
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58.2%; Score 39; DB 5; Length 275;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dobson K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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                                                                                                                                              STRAIN=VF39;
MEDLINE=99113394; PubMed=9914965;
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01-FEB-1997 (TrEMBLrel. 02, C3
01-AUG-1998 (TrEMBLrel. 07, L4
01-DEC-2001 (TrEMBLrel. 19, L4
F53H4.4 protein.
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01-JUN-2002 (TrEMBLrel. 21, C2
01-JUN-2002 (TrEMBLrel. 21, L6
01-JUN-2002 (TrEMBLrel. 21, L6
VOMERONASAI receptor VIRE6.
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Best Local Similarity 60.00,
6; Conservative
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245 RWLRNLRKLR 254
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NCBI_TaxID=387;
                                                       STRAIN=VF39;
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QBR2A4 ESULT 8 8R2A4

us-09-743-107b-88.rspt

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Nature 402:761-768(1999).
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STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                      Local Similarity
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les 6; Conserv
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501 QWFRNMKK 508
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STRAIN=COLUMBIA;
MEDLINE=9393451; PubMed=10470850;
MEDLINE=9393451; PubMed=10470850;
Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
Structural analysis of Arabidopsis thaliana chromosome S. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen
Pl and TAC clones.";
Pl and TAC clones.";
SEMBL; A8018113; BAB091751; -
SEQUENCE 866 AA; 100187 MW; 164FAB9B4976D27D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STELLA D.ORO; TISSUE-SENESCING PETALS; MEDLINE=9933248; PubMed=10412903; MEDLINE=9933248; PubMed=10412903; Panavas T., Pixula A., Reid P.D., Rubinstein B., Walker E.L.; "Identification of senescence-associated genes from daylily petals.";
                                                                                                                                                                                                                                         Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales,
Hemerocallidaceae, Hemerocallis.
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1-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Senescence-associated protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-070-2002 (TrEMBLrel. 21, Created) 01-070-2002 (TrEMBLrel. 21, Last sequence update) 01-070N-2002 (TrEMBLrel. 21, Last annotation update) Hypotherical 12.3 kDa protein.
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Best Local Similarity 60.0
Matches 6; Conservative
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STRAIN=STX2 PHAGE-I;
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MEDILISE_20083487; PubMed=10617197;
MEDILINE_20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee U.J., Ronning C.M., Koo H., Woffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Misman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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EMBL, AC007170; AAD25641.1; -
InterPro; IPR004264; Transposase_23.
Pfam; PPG01717 Transposase_23; 1.
SEQUENCE 531 AA; 60512 \( \bar{M}M \); 57B3AC60C976A4B9 \( \text{CRC64}; \)
Plant Mol. Biol. 40:237-248(1999).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL. AF082028; AAC34853.1; -.
PITHEAPRO; 1PR091128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00365; P450.
PROSITE; P500086; CYTOCHROME P450; UNKNOWN_1.
NON_TER 1
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Last annotation update)
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Q77855, (T.EMBLrel. 01, Created)

01-NOV-1996 (T.EMBLrel. 01, Last sequence update)
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K MEDLINE=55191002; PubMed=7884975;

Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,

Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;

Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;

"Similarity in env and gag genes between genomic RNAs of human immundeficiency virus type 1 (HIV-1) from mother and infant is in unrelated to time of HIV-1, RNA positivity in the child.";

J. Virol. 69:2285-2296(1995).

R EMBL, 247967; CAA87881.1; -..

R InterPro; IPRO0777; GP120.

R Pfam; PF00516; GP120, 1...

AIDS; Coat protein; Glycoprotein.
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Best Local Similarity 60.0%; Pred. No. 9.9;
Matches 6; Conservative 2; Mismatches 2; Indels
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                         Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VCBI_TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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earch completed: February 21, 2003, 08:00:43 ob time: 22.6744 secs

3 QWXRNMRKVR 12 || | ::||| 67 QWDRTLQKVR 76

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                                                                                                                                                                       February 21, 2003, 07:37:21 ; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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| SIDS2/gcdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
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AAY78038
AAY78046
AAY78086
AAY78089
AAY78090
AAY78037
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Gapop 10.0 , Gapext 0.5
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BO	Human 1	actof	errin d	erived		peptide SEQ ID NO:7.		
¥\$\$\$\$	XX KW Human; I KW food; ir KW urinary KW bacteric	lactof nfant tract	errin; m formula; infecti preserv	odi an on;	. 01:0	tion, infection; nflammatory; anti itis; Candida inf	inflammat: -microbial ection; fu	lon; tumour; l; anti-tumour; ingicidal;
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1	(ASCI-)	A+ SCI	I INVEST	ST AB				
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Conservative
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Best Local Similarity
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29-DEC-1998;
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                                                               AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food sruffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 5.3e-05;
0; Mismatches 1; Indels
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                                             Claim 22; Page 35; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           AAY78038 standard; Peptide; 12 AA
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 7.9e-05;
0; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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ilarity 91.7%;
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through ladiding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as uninary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                      Score 64; DB 21; Length 12;
Pred. No. 7.9e-05;
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AAY78090 standard; Peptide; 12 AA.

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                                                                                                                                                                                food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal; bactericidal, preservative.
                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.0%; Score 64; DB 21; Length 12;
100.0%; Pred. No. 7.9e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:89.
                                                                                                                                                                                                                                                                                                                                                                                                          Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 37; 102pp; English.
                                                                             AAY78089 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                          Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                   98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                          (first entry)
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
                  1 CPOWOREMRKVR
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17-JUL-1998;
29-DEC-1998;
                                                                                                                         25-APR-2000
                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as uninary tract inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Local Similarity 100.0%; Pred. No. 7.9e-05;
hes 12; Conservative 0; Mismatches 0;
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                                                                                                    Human lactoferrin derived peptide SEQ ID NO:90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 37; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY78090;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have deelared anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
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Best Local Similarity 91.7
Matches 11, Conservative
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Dolphin GT;

Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                                                           Dolphin GT
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                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 74; 102pp; English.
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                                                                                              99WO-SE01230.
                                                                                                                             98SE-0002441
98SE-0002562
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                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
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Matches 11; Conservative
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                                                                                              06-JUL-1999;
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0; Gaps

Score 64; DB 21; Length 13; Pred. No. 8.6e-05; 0; Mismatches 1; Indels

97.0%; 91.7%;

13 AA;

(first entry)

99WO-SE01230

06-JUL-1999;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane) inflammations, collifis, and candid anidetion on a mucosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also been the candidal and may also be used as preservatives.
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 8.6e-05;
0; Mismatches 1; Indels
                                                                                                          Dolphin GT
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                                                                                                        Baltzer L,
                                                                                                                                                                                                               Claim 18; Page 74; 102pp; English
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             98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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91.78;
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                                                                          (ASCI-) A+ SCI INVEST
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                                                                                                                                      WPI; 2000-147388/13.
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             06-JUL-1998;
17-JUL-1998;
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                                          Hanson LA,
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment or through the direculation. A medicinal product of the peptide or fragment or be used for treating and/or prevention of infections (such as unimary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower periods.
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food; infant formula, anti-inflammatory; anti-microbial; anti-tumourinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                           New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 64, DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                           Claim 12; Page 69; 102pp; English.
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91.7%;
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98SE-0004614.
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nes 11; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    3 CFOWORNMRKVR
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                            AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory, anti-microbial; anti-tumour,
utinary tract infection, colitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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Claim 15; Page 75; 102pp; English.
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91.7%;
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98SE-0004614.
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Matches 11; Conservative
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urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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1 Similarity 91.7%;
11; Conservative
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Matches 11; Conservative
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ID AAY7
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AC AAY7
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Human lactoferrin derived peptide SEQ ID NO:35.
25-APR-2000 (first entry)
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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens Synthetic. WO200001730-A1.

13-JAN-2000.

99WO-SE01230. 06-JUL-1999; 98SE-0002441. 98SE-0002562. 98SE-0004614. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

(ASCI-) A+ SCI INVEST AB.

Baltzer L, Dolphin GT; Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 69; 102pp; English

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all initically on a broad basis because of high production costs. Therefore, provision of peptides because of high production enable them to be used for the same purposes as lactoferrin at lower

15 AA; Seguence

. 0 Query Match

97.0%; Score 64; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels

1 CFOWORXMRKVR 12

4 CFOWORNMRKVR 15

g 8

Search completed: February 21, 2003, 07:56:43 Job time: 28.093 secs

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Sequence
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GENERAL INFORMATION:
APPLICANT: YAWARATION:
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATRAU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: UCHIDA, TOSHIMINO
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: VIRAL INPERTION:
TITLE OF INVENTION: VIRAL INPERTION
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATEMY ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
ADDRESSEE: THIBEAULT
ADDRESSEE: MA
COUNTRY: USA
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CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIRE: OCNAMINE: TOSH
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LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTONEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/POCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7100
INFORMATION POR SEQ ID NO: 3:
SEQUENCE CRARACTERISTICS:
LENGTH: 18 amino acids
TWANDER: AMINO acids
TELENGTH: 18 amino acids
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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                                                                                                                                                February 21, 2003, 07:50:40; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 6,
Sequence 6,
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Sequence 24
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Sequence 4,
Sequence 6,
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Sequence 1,
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Sequence 1
Sequence 7
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Sequence
Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:*
. /cgn2 6/ptodata1/iaa/5A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/5B_COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/6A_COMB.pep:*
. /cgn2 6/ptodata1/iaa/RB_COMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
. /cgn2 6/ptodata1/iaa/PCTUS COMB.pep:*
                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-07-755-161h-3
US-08-264-71-24
US-08-266-771-25
US-08-381-984-24
US-08-381-984-24
US-09-568-734-4
US-09-568-734-6
US-09-568-734-6
US-09-568-734-6
US-09-568-734-6
US-09-568-734-6
US-09-568-734-8
US-09-568-734-8
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US-09-568-734-8
US-09-568-734-8
US-09-268-734-8
US-09-268-734-8
US-09-268-734-8
US-09-268-734-8
US-09-268-734-8
US-09-268-734-8
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                                                                                                                                                                                                                                                                                                                                                                                      262574 segs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       M protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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66
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                                                                                                                                                                                                                                                                              1 CFOWORXMRKVR 12
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atabase:
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US-08-475-055-8
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APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: RNDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES:
ADDRESSPE: Klauber & Jackson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.0%; Score 64; DB 2; Length 18; Best Local Similarity 91.7%; Pred. No. 3.8e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                     Length 18;
                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: 1411 Hackensack
STATE: New Jersey
COUNTER: USA
ZIP: 07601
COMPUTER REABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                       Score 64; DB 1; 1
Pred. No. 3.8e-05;
                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE:
CLASSIFICATION 1916
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,343-1684
                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOHNSON INDEAL TOPOLOGY: INDEAL MOLECULE TYPE: peptide DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
) OTHER INFORMATION:
US-08-204-487-3
                                                                                                                                                               1 CFQWQRXMRKVR 12
                                                                                                                                                                                                            CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-485-948-8
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Gaps

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GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: CERAM, HELEN
APPLICANT: CERAM, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                            ADDRESSE: Klauber & Jackson STREET: All Hackensack Avenue CITY: USA STATE: New Jersey COUNTRY: USA ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: ISM PC COMPATIBLE OF COMPUTER: HACKEN: PAPLICATION DATA:
APPLICATION NUMBER: US 08/628,380
FILING DATE: April 4, 1996
FLING APPLICATION S14
REIGN APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELESCIETRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELESCOMMUTICATION INFORMATION:
TELESCOMMUTICATION INFORMATION:
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
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Application US/08628380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: ENDPROD
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFÓWORNMRKVR 12
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" UBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.0%; Score 64; DB 1; Length 20;
                                  SULTIMARE: LIBERAYALICE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR PAPPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WATTEN NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
mm FOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: AMINO ALID STRANDEDNESS: single
    OPERATING SYSTEM: MS-DOS
                       DisplayWrite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUB TYPE:
CELL IYPE:
CELL LINE:
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ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-755-161A-3
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Pred. No. 3.8e-05;
0; Mismatches 1; Indels
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Fatent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10 Antimicrobial Agent NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: SOS Fifteenth Street, N.W., #700 CITY: Washington STREET: 10.5.A.
STATE: U.S.A.
ZARIE: U.S.A.
ZARIE: U.S.A.
ZIP: Z0005
COMPUTER READBLE FORM:
MEDIUM TYPE: IBM Compatible
                                                                                                                 ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRANT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/418,217
FILING DATE: JUNE 7, 1995.
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995.
CLASSIFICATION: ALTONEY, 1995.
ALTONEY/AGENT INFORMATION:
NAME: JACKSON ESG., DAVIG AREPRENCE/DOCKET NUMBER: 947-1-00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE: 201 343-1684
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: internal JS-08-475-055-8
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JS-07-755-161A-3
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with PUBLICATION INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
ATTHORS:
ATTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAVASHINA, HIDEKI
APPLICANT: NAVASHINA, HIDEKI
APPLICANT: NOSUCHI, WATRAU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: KAMASAKI, YOSHIHIRO
APPLICANT: KHANSAKI, YOSHIAKI
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

2.TP:

COUNTRY READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INPORMATION:

NAME: CAMPBELL, PAULA A.

REGISTRATION NUMBER: 32,503

REFERENDES/COCKET NUMBER: FJN-019

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08204487; Patent No. 5565425
GENERAL INFORMATION:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISSUE:
PAGES:
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                                                                                              Gaps
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                                                                                           Indels
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Sequence 3, Application US/07891174
Sequence 1. Application US/07891174
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Warderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 2006
CONFUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATION SYSTEM: MS.DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 05-SEP-1991
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/755,161
ATTORNEY/AGENT INFORMATION:
ARFERENCY/DOCKET NUMBER:
TELECOMMUNICATION NUMBER:
TELEFROME NUMBER:
                                                             Pred. No. 4.2e-05;
0; Mismatches 1;
                                                          Best Local Similarity 91.7%;
Matches 11; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FEATURE:
NAME/KEY: modified site
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL ITYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                      1 CFOWORXMRKVR 12
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CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                          2 CFÓWORNMRKVR 13
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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US-07-891-174-3
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2 CFOWORNMRKVR 13
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US-08-381-984-24
            US-08-256-771-24
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Sequence 24, Application US/08256771
Fatent No. $66567
Fatent No. $6667
Fatent 
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97.0%; Score 64; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                             NAME/KEY: Peptide | LOCATION: 1.20 | LOCATION: 1.20 | COTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE | CTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN" | JS-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEX/AGENT INPORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERSINCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRXMRKVR 12
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ilarity 91.7%; Pred. No. 4.2e-05;
Conservative 0; Mismatches 1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acide
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                   1 CFQWQRXMRKVR 12
                                                                                                                                                                                                       2 CFQWQRNMRKVR 13
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US-08-256-771-25
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RESULT 12
US-08-208-34-4
; Sequence 4, Application US/09508734
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION;
APPLICANT: Samyang Genex Corporation
; TITLE OF INVENTION: Useful microorganism thereof
; TITLE OF INVENTION: UNMERR: USO0-06-01
; FRIOR APPLICATION NUMBER: USO9-07-14
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KOPATENTION 1.71
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LOCATION:
LOSTHIPECATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
FEATURE:
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IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: JS-DRICK APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: WATER WATER M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
TELEPAN:
TELEPAN:
TELEPAN:
                                                                                                                                                STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CFQWQRXMRKVR 12
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                                                                                                                                                                                                                                                 COUNTRY:
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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Sequence 24, Application US/08381984

Patent No. 2804555

Patent No. 2804555

TOTOREL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.

COUNTRY: U.S.A.

ZIF: 20005

COMPUTER PROPERTY: COMPUTER PROPERTY

ZIF: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER 12003
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: I BE Compatible
COMPUTER: I BE Compatible
COMPUTER: I BE COMPACE:
COMPUTER: WAS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION:
APPLICATION NUMBER:
FILING DATE:
ATTORNAY AGENT:
ATTORNAY AGEN
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Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
COMBESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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Matches 11; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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NAME/KEY:
LOCATION:
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STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and

TITLE OF INVENTION: Useful microorganism thereof

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: DC/00-06-01

PRIOR PILING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

SETOR APPLICATION NUMBER: KR1998-29351

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

LENGTH: 24
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                                                                                               Query Match

97.0%; Score 64; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
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158-07-755-161A-10

Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

Patent No. 5304633

Fatent No. 5304633

TITLE OF INVENTION: Antimicrobial Peptides and TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Washington

CITY: Washington

STATE: D.C.
COMPTRY: U.S.A.

ZIP: 2005

COMPTRY: U.S.A.

ZIP: 2005

COMPUTER: EDISKEtte, 5.25 inch, 500XD

COMPUTER: Diskette, 5.25 inch, 500XD

COMPUTER: DisplayWrite

CURRENT APPLICATION DATH:
APPLICATION NUMBER: US/07/755,161A

TITLE DISPLAYED

TITLE OF INVENTION NUMBER: US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                   TYPE: PRT
CORGANISM: Homo sapiens
JS-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
JS-09-508-734-6
                                                                                                                                                                            1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                    2 CFOWORINMRKVR 13
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JS-09-508-734-6
LENGTH: 22
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WANTERNAY AGENT TROOMATON:

WANTERNAY AGENT TROOMATON:

WANTERNAY AGENT TROOMATON:

WANTERNAY AGENT TROOMATON:

TELEBOOKS: 202-311-8850

TELEBOOKS: 202-211-8850

TELEBOOKS
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Search completed: February 21, 2003, 08:04:26 Job time : 9.93023 secs
                                                                                                                                                             JOURNAL:
JOURNAL:
VOLUME:
SSUE:
PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.0%;
Best Local Similarity 91.7%;
Matches 11; Conservative
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LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
RESULT 15
UG-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: 805 Fifteenth Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington STATE: D.C.
ZIP: 20005
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NUMBER: US 07/755,161
PRICE COMPUTER: NOWERE: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUTER: TELECOMMUTER: TELECOMMUTER:
TELECOMMUTER: TELECOMMUTION: TELEFAX: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified site 21
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HYPOTHETICAL:
HYPOTHETICAL:
ANTI-SERME:
RAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL TYPE:
ORGANELLE:
ORGANELLE:
IMMEDIATE SOURCE:
LINE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
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LOCATION:
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IDENTIFICATION METHOD:
OFFER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS;
TITLE:
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0
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Pred. No. 5.2e-05;
0; Mismatches 1; Indels
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Sequence 1 Sequence 1

Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 715, Ap Sequence 5715, Ap Sequence 7715, Ap Sequence 7715, Ap Sequence 7, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 25, Appli Sequence 25, Appli Sequence 25, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 28, Appli

Sequence 4,

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Query Match
97.0%; Score 64; DB 9; Length 15;
Best Local Similarity 91.7%; Pred. No. 2.5e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
0 US-09-904-536-14

0 US-09-904-536-15

0 US-09-904-536-16

0 US-09-904-536-10

0 US-09-904-536-10

0 US-09-904-536-10

0 US-09-904-536-10

0 US-09-904-6

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0 US-09-764-864-1031

0 US-09-764-864-1031

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0 US-09-768-869-5

0 US-09-90-453A-2

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US-09-798-869-25
US-09-798-869-11
US-09-798-869-10
US-09-798-869-28
US-09-798-869-24
US-09-798-869-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: (VSTEIN REKDAL

APPLICANT: (VSTEIN REKDAL

APPLICANT: LARS VORLAND

ITTLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT PILING DATE: 1999-08-31

PRIOR PILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PASSESQ for Windows Version 4.0

SEQ ID NO :

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
    ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORXMRKVR 12
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    US-09-798-869-20
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Sequence 23, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 8, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 4,7985, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
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2, Appli
6, Appli
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23, Appli
23, Appli
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22, Appli
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                                                                                            February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
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Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*

| CGTAZ 6 (prodata/2/pubpaa/USOB NEW PUB.pep:*
| CGTAZ 6 (prodata/2/pubpaa/USOF PUBCOMB.pep:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-023-096-2
US-09-798-869-6
US-09-798-869-3
US-09-798-869-3
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-29
US-09-798-869-29
US-09-798-869-29
US-09-798-869-30
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US-09-904-536-9
US-09-904-536-11
US-09-904-536-12
US-09-904-536-13
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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66
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                                                                                             Run on:
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Query Match 97.0%; Score 64; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.00096; Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                          1 CFOWORXMRKVR 12
                                                                                                                                                    22 CFOWORNMRKVR 33
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US-09-798-869-3
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LENGTH: 15
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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Tomaaz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh &t. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.0%; Score 64; DB 9; Length 25; Best Local Similarity 91.7%; Pred. No. 4.1e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
APPLICANT: LARS VORLAND.

TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-WAY-1994
ATTORNEY APPROPER INFORMATION:
NAME: PLAYER, WILLIAM E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/F5816
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQRXMRKVR 12
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Gaps
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Pred. No. 0.00062;
0; Mismatches 2; Indels
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                                                                                                                                                                                 JUNE OF 1798-869-6

Sequence 6, Application US/09798869

Publication No. US20030022821A1

PUBLICANT: JOHN SIGURD SYENDSEN

APPLICANT: JOHN SIGURD SYENDSEN

APPLICANT: ALSE VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT PILING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: PCT/GB99/02851

PRIOR APPLICATION NUMBER: GB9818938-4

PRIOR PILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PSEUSEC for Windows Version 4.0

SEC ID NO 6

LENGTH: 15
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; Publication No. US2003002281A1
; GENERAL INFORMATION:
APPLICANT: OJOHN SIGUED SVENDSEN
; APPLICANT: OYERN REMOAL
; APPLICANT: HARS VOEINBUR SVEINBLARSON
APPLICANT: HARS VOEINBUR SVEINBLANSON
APPLICANT: HARS VOEINBUR SVEINBLARSON
TILLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
SOFTWARR: PARESEQ for Windows Version 4.0
SOFTWARR: PARESEQ for Windows Version 4.0
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Best Local Similarity
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63.6%; Pred. No. 0.12;
11ve 1; Mismatches
                                                                                                                                                                                                                          PAPLICATION NO. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDERN
APPLICANT: JOHN SIGURD SVENDERN
APPLICANT: BALDUR SVEINBJ(RNSCN)
APPLICANTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A44049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAEESEQ for Windows Version 4.0
SEQ ID NO 4
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDERN
APPLICANT: ALLOW SIGHED SVENDERN
APPLICANT: ALLOW SUSING FREAD.
ITLE OF INVENTION: BIOACTIVE PEFTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 1090-09-798, 869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE9818938.4
PRIOR PLING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREUSED for Windows Version 4.0
SEQ ID NO 2
LENGTH: 25
TYPE: PRT
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity
          1 CFQWQRXMRKV 11
                                                                     3 CYÓWÓWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWORXMRKV 11
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; ORGANISM: MURINE
US-09-798-869-4
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US-09-798-869-22
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88.2%; Score 45; DB 9; Length 15;
Best Local Similarity 63.6%; Pred. No. 0.051;
Matches 7; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 53; DB 9;
Pred.'No. 0.0034;
2; Mismatches 1
                                                                                                                                                                                                            RESULT 6
18-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US2003002281A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN RENDAL
APPLICANT: (YSTEIN RENDAL
APPLICANT: HALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOUTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO. SE
   2; Mismatches
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Publication No. US20030022821A1
GENERAL INPORMATION:
APPLICANT: USTEIN REKDAL
APPLICANT: GYSTEIN REKDAL
APPLICANT: HALDON SVENDSEN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACE FRACE OF UNION STATES
TENTIOR TILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACE FRACE OF UNION STATES
TENTIOR TILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACE FRACE OF UNION STATES
TENTIOR TILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACE FRACE OF UNION STATES
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Best Local Similarity 72.7°
8; Conservative
                                                                 1 CFOWORXMRKV 11
                                                                                                                            3 CYQWQRRMRKL 13
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ORGANISM: CAPRINE
IS-09-798-869-23
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Matches
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Sequence 30, Application US/09798869
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; ORGANISM: BOVINE
US-09-798-869-30
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US-09-864-761-47985
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US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.1%; Score 41; DB 9; Length 15; Best Local Similarity 63.6%; Pred. No. 0.26; Matches 7; Conservative 1; Mismatches 3; Indels
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                                                                                PUBLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REXDAL RNSSON
APPLICANT: (YSTEIN REXDAL RNSSON
APPLICANT: BALDUR SVELNBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEFTIDES
FILE REFERENCE: A34049-FOT-USA-A
CURRENT FILING DATE: 1999-00-31
PRIOR PLING DATE: 1999-00-31
PRIOR FILING DATE: 1999-00-31
PRIOR FILING DATE: 1999-00-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NOS: 30
SEQ TRANKE: FASTESEQ FOT WINDOWS Version 4.0
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: GYSTEIN REEGAL
APPLICANT: BALDUR SVEINBJ (RNSON)
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A14049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1996-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESESE 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESESE 1998-08-38
                                           Sequence 8, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 6; Conserv
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US-09-798-869-29
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US-09-798-869-29
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3 CFRWÓWRMKKL 13

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RESULT 12 US-09-798-869-30

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GENERAL INFOGRATION:
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERBNCE: Acomica.X. 1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0066
PRIOR PRIOR PLING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 9;
Pred. No. 0.26;
3; Mismatches
                                                   APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBAL
APPLICANT: BALDUR SVEINBAL
APPLICANT: BALDUR SVEINBAL
REKDAL
TITLE OF INVENTION: BIOACITYE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: PastSEQ for Windows Version 4.0
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APPLICATION NUMBER: PCT/US01/00662
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Patent No. US20020048763A1
GENERAL INFORMATION:
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54.5%;
US20030022821A1
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Best Local Similarity 54.5
Matches 6; Conservative
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APPLICANT: Barry III, Clifton E.

APPLICANT: Bearry III, Clifton E.

APPLICANT: DeBarber, Andrea E.

APPLICANT: Maluli, Knisimuzi

APPLICANT: Bekker, Linda-Gail

APPLICANT: Beresented by The Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis

FILE REFERENCE: 012504-41310US

CURRENT APPLICATION NUMBER: US 60/214,187

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGHH 489
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OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
15-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXT.HUMAN HIT: AM294800.1, EVALUE 1.00e-06
IS-09-864-761-47985
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Pred. No. 1.8;
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           PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR PILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-09-21

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR PILING DATE: 2001-01-29

NUMBER: OF SEQ ID NOS: 49117

SEQ ID NO 47985

LENGTH: 21
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2001-01-30
NITMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFORMATION:
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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16 CFQWRR 21
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Sequence 8, Application US/09904536 Patent No. US20020111475A1 GENERAL INFORMATION:

ESULT 15 S-09-904-536-8

253 COKWPRRMRKM 263

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APPLICANT: Graddis, Thomas J.

TITLE OF INVENTION: PLT3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/904,536

CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR PLICATION NUMBER: PRIOR APPLICATION: 09/109,100
PRIOR FILING DATE: 1399-07-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 209

TYPE: PRT

ORGANISM: Homo sapiens

US-09-904-536-8

Query Match
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps

Qy 1 CFOMORARR 10

Db 178 CLHWQRTRRR 187

Search completed: Pebruary 21, 2003, 08:11:55
JOB time: 6.88372 secs
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version 5.1.3 - 2003 Compugen	; Sear	* 0/.	ហ	residues	parameters:	ıries		predicted by score of the otal score d	SUMMARIES																			- a		
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fprA protein - Myx hypothetical prote cell cycle arrest ornithine decarbox probable cytochrom cytochrome P450-1i cytochrome P450-1i cytochrome P450-1i cytochrome P450-1i cytochrome P450-no hypothetical prote finger protein unk hypothetical prote kinase-related pro protein F21H11.2 [carcinoembryonic a	S 1-1997 #text change 08-Dec-2000 \$15853; \$20841; \$07160; A61169; A3100 4 1L/DDBJ PIDN:AAB60324.1; PID:G467237 eper, F.R. In mammary gland lactoferrin.
T10126 AD2346 A39654 S52784 B96691 B85441 T04730 C85441 T24214 T24216 S42226 B42226 A35774 D89450	- huma - huma - 10324; rch 199 - rch
0000000000000000	n n n n n n n n n n n n n n n n n n n
270 298 306 4306 431 492 492 500 500 511 511 614 614 2594 2700	sor [v ofean; ofean; ofean; illes; illes; illes; crans] trans] trans]
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	pre 33:1 3920; 3942; 1944 1944 1947; 1948; 1947;
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U U U U U U U U U U U U U U U U U U U	RESULT 1  TEHUL  lactotransferrin precursor [v. Species: Homo sapiens (man) C. Species: Homo sapiens (man) C. Date: 31-Mar-1992 #sequence C. Accession: G01394; 511228; R. Cho, Y. Submitted to the EMBL Data Li A, Reference number: G06820 A, Reference number: G06820 A, Reference number: G06820 A, Residues: preliminary; transl A, Nolecule Fype: mRNA A, Residues: 1-71 cCNO A, Cross-references: EMBL:U076 R, Rey, M. W. Wolselwuk, S.L.; Nucleic Acids Res. 18, 5288; A, Title: Complete nucleotide A, Reference number: S11228; PA, Ricession: S11228; PA, RACESSION: S11228
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lactotransterrin precursor [validated] - human N:Alternate names: lactoferrin	
C; Species: Homo sapiens (man)	,
C,Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000 C,Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169;	-Dec-2000 0; A61169; A31000; S74
R;Cho, Y. submitted to the EMBL Data Library. March 1994	
tumber: G06820	
A;Accession: G01394 A:Status: preliminary: translated from GB/EMBL/DDBJ	
A, Molecule type: mRNA	
Ajkebiques.i-/l ccho. a.fraesiques-references EMRI.HO7643. NID.a467236. DIDN.aarch324 1. DID.a467237	1.0467237
7 7 7 7	
Nucleic Acids Res. 18, 5288, 1990	
A;Title: Complete nucleotide sequence or numan mammary giand lactorerin. A:Reference number: S11228: MUID:90384839: PMID:2402455	nerrin.
A, Accession: S11228	
A; Molecule type: manA	
A;kesidues: 1-148,'1',150-422,'C',424-711 <kex> A:Cross-references: EMBL:X53961: NID:c34415: PIDN:CAA37914.1: PID:c34416</kex>	934416
lmer, D.; Panella, T.	
A)Title: Differential molecular mechanism of the estrogen action that regulates	hat regulates lactoter
A.A.C.C.C.C. MANAGET STORES FOR STORES AND S	
A; Molecule type: DNA	
	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312	263312
A;Experimental Bource: placenta A:Note: semience extracted from NCBI backbone (NCBIP:122202)	
A, Title: Nucleotide sequence of human lactoferrin cDNA.	
A;Reterence number: S10324; MUID:90326549; PMID:2374734	
A.Molecule type: mRNA	
A, Residues: 3-711 <pow></pow>	
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412 R:Stowell, K.M.: Rado, T.A.: Fink, W.D.: Tweedie, J.W.	934412
Biochem. J. 276, 349–355, 1991	
A, Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.	cell
A;Reference number: S15853; MUID:91264/86; PM1D:2049056 A;Accession: S15853	
cid sequence not shown; not compared with conceptual	ptual translation
A, Residues: 20-31 <st1></st1>	
A;Accession: S20841 A:Molecule type: protein	
A, Residues: 20-28, 'X', 30-31 <st2></st2>	

Length 708

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Score 53;
Pred. No.
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Best Local Similarity 63...
7; Conservative
                                                   Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; divorprotein; iron binding; milk
F; Cypeywords: duplication; glycoprotein; iron binding; milk
F; Cypeymodis: signal sequence #status predicted <SiGo*
F; Cypeymodis: signal sequence #status experimental <MAT>
F; Cypeymodis: transferrin repeat homology <TRHI>
F; Cype (699/Domain: transferrin repeat homology <TRHI>
F; Cype (699/Domain: transferrin repeat homology <TRHI>
F; Cype (699/Domain: transferrin repeat homology <TRHI>
F; Cype (699/Disulfide bonds: #status epsilogy of Cype (Cype 
                                                                                                                                                                                            A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 436-487, 48, 489-711 cRAD>
A, Gross-references: BMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
A; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
A; Alticle: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth, A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: UC2323
Accession: UC2323; MUID:9438047; PMID:8093048
A; Fitle: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A; Reference number: UC3323; MUID:94380447; PMID:8093048
A; Reference number: UC3323
A; Accession: UC3223
A; Accession: UC3223
A; Reference number: UC3233
A; Reference number: UC3333
A; Reference number: UC3333
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: protein
Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-
Note: this is the final paper in a series
Note: this is the final paper in a series
Although, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.
Although, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.
Although, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.
           Altitle: Isolation of lactoferrin cDNA from a human myeloid library and expression of AlReference number: S07160, MUID:88001031; PMID:3477300
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pate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
Accession: JC2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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91.7%; Pred. No. 0.00083;
tive 0; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 3-701,'SWKPVN' <PAN>
A;Experimental source: 100 normal breast tissue
R;Metz-Boutigue, M.H.; Jolles, J.; Maxurier, J.; Schoentgen,
Eur. J. Blochem. 145, 659-666, 1984
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A;Residues: 'G', 23-24,'R', 26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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Rado, T.A.; Wei, X.; Benz Jr., E.J.
lood 70, 989-993, 1987
Title: Isolation of lactoferrin cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 CFÓWORNMRKVR 50
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nes 11; Conserv
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C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
D. Biol. Chem. 262, 10134-10139, 1987
A;Fitle: Lactotransferrin is the major estrogen inducible protein of mouse uterine secré
A;Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an inhibitor of platelet
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                                                                                                                                                                                                                                lactoferrin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-01-1959$ #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Readidues: 3-707 - CPEN>
A,Cross-references: BMBL-003298
R,Liu, Y.; Teng, C.T.
J. Baiol. Chem. 266, 21880-21885, 1991
A,Fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A,Reference number: A41205, MUID:92042099, PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Gaps
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Fill9/Domain: signal sequence #status predicted <MAT>
Fill9/Domain: lactotransferrin #status predicted <MAT>
Fill88-655/Domain: transferrin repeat homology <TRH2>
Fill94/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 3.6;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 33;
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A, Molecule type: DNA
A, Residues: 1-15 < LIUD.
A), Cross-references: GB: M74778
C; Superfamily: transferrin; transferrin repeat homology
C; Keywords: duplication; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 1.33 Q1AA
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
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Pred. No. 0.016;
      2; Mismatches
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Gaps

Gene: ODA4 Genetics:

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RESULT 8
H97451
pyrdokamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (str C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Accession: H97451
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum. A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell, Kary, P.; Romerov, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authorg: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Duj C;Species: Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: H97451
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-206 «KUR»
A;Cross_references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
R;Favello, A.; Gattung, S. subrary, March 1996
subaltred to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
A;Reference number: Z20528
A;Reference number: Z20528
A;Acession: T28820
A;Status: prelimary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-932 <FAV>
A;Residues: 1-932 <FAV>
A;Residues: BMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 60.6%; Score 40; DB'2; Length 932; Best Local Similarity 63.6%; Pred. No. 25; Matches 7; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 206;
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Pred. No. 9;
2; Mismatches 4
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A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 50.0%;
Matches 6; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 FÓWÓRSARLVK 589
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A,Molecule type: DNA
A,Residues: 1-206 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: CESP:F07C3.1
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                                                                                                                                                                        ynein beta heavy chain - Chlamydomonas reinhardtii

'Species: Chlamydomonas reinhardtii

'Jate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001

'Mitchell, D.R., Brown, K.S.

Cell Sci. 107, 635-644, 1994

'Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.

'Reference number: 216302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map position: IX

introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;

introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1115/3;

introns: 48/2; 3868/3; 4240/3

introns: 48/2; 3868/3; 4240/3

introns: 48/2; 38/3; 1004/3; 1115/3;

introns: 48/2; 1106/3; 1106/3; 1106/3; 1115/3;

introns: 48/2; 1106/3; 1106/3; 1115/3;

introns: 48/2; 1106/3;

introns: 48/2;

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Nolecule type: DMA
Residues: 1-275 cML
Cross-references: EMBL.Z81089, PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
Experimental source: clone F53H4
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: translated from GB/EMBL/DDBJ
Molecule type: DNA
;Residues: 1-4568 «MIT»;
;Cross-references: EMBL:U02963; NID:9409965; PIDN:AAA19956.1; PID:9514215
;Experimental source: strain 21gr
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;Introns: 67/1; 153/1
;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.2%; Score 43; DB 2; Length 4568; 50.0%; Pred. No. 32; arive 3; Mismatches 3; Indels
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60.6%; Score 40; DB 2; Length 275;
Best Local Similarity 63.6%; Pred. No. 7.8;
Matches 7; Conservative 1; Mismatches 3; Indels
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Best Local Similarity
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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; K.; Kaul, S.; Rounsley, S.D.; Shaa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Coo, H.; Moffat, K.S.; Cronin, L.S.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, v. Aritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID:20083487; PMID:10617197
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Molfet, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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C; Species: 0.1-Fb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C; Accession: T00513; F84621
R; Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997
A; Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence. A; Reference number: 214164
                                                                                                                                                                                                                                                                                                                                                                                                            probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thallana (mouse-ear cress)
Cjapecies: Arabidopsis thallana (mouse-ear cress)
Cjatcesion: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
Cjaccession: T00510; A84622
RjRounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence.
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A;Introns: 182/3; 310/3
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Reywords: heme; iron; metalloprotein
C;Reywords: heme; iron; metalloprotein
F;312-471/Domain: cytochrome P450 homology <P45>
F;349/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A, Cross-references: GB: AE002093; NID: G2642441; PIDN: AAB87109.1;
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               Length 289
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-515 «ROUS
A;Residues: 1-515 «ROUS
A;Cross-references: EMBL:AC002391; NID:g2642427; PID:g2642441
A;Experimental source: cultivar Columbia
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Pred. No. 33;
1; Mismatches
               DB 2;
19;
               Score 38; DB 2
Pred. No. 19;
1; Mismatches
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A;Molecule type: DNA
                   57.6%;
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ilarity 83.3%;
Conservative
               Query Match 57.6
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: At2g23220; T20D16.15
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                                                                                                                                                                                                                                 8 CFTWEEYARHVR 19
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                   CFOWORXMRKVR
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T00513
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Ritheologis, A.; Bcker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.J.; Chung, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.K.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Alauthors: Hunter, J.D.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Alauthors: Salzberg, S.L.; Sakano, H.

Alauthors: Salzberg, S.L.; Panatziali, R.M.

Alauthors: Salzberg, S.L.; Panatziali, R.M.

Alauthors: Speluminary

Alauthors: Speluminary

Alauthors: Speluminary

Alauthors: Speluminary

Alauthors: Salzberg, S.L.; Sakano, H.

Alauthors: Speluminary

Alauthors: Salzberg, S.L.; C.M.; Venter, J.C.; Davis, R.W.

Alauthors: Speluminary

Alauthors: Salzberg, S.L.; C.M.; Venter, J.C.; Davis, R.W.

Alauthors: Salzberg, S.L.; Sakano, H.

Alauthors: Salzberg, S.L.;
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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P. Mazur, M.; Goltsman, E.; Selkov, T.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Nazur, M.; Goltsman, E.; Selkov, T.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese A; Mazur, M.; Acd. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:1175668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable pyridoxamine-phosphate oxidase (BC 1.4.3.5) [imported] - Brucella melitensis (q
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A,Molecule type: UMS
A,Residues: 1-208 «KUR»
A;Cross_references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
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A;Cross-references: GB:AE008688; PIDN:AAL41776.1; PID:g17739129; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:
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C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
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Pred. No. 9;
2; Mismatches
                                                                                                                                                                                                                                                                        59.1%; Score 39; DB 50.0%; Pred. No. 9; ative 2; Mismatches
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C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
                                                                                                                        A,Gene: pdxH
A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 50.0
Matches 6, Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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A, Map position:
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Search completed: February 21, 2003, 08:02:44
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Superfamily: phytochrome; phytochrome homology
Keyworze chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
Keyworze chromoprotein; dimer; photosceptor; phytochrome homology <PHY>
(55-581/Domain: phytochrome homology <PHY>
(321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T14803
Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet, bmitted to the EMBL Data Library, April 1996
Accession: T14803
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Note: this species has also been called Salmonella typhi
Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

    Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
ence number: A84420; MUID:20083487; PMID:10617197

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                                                                                                                                                           Molecule type: DNA
Residues: 1-543 <STO>
Cross-references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139
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Pred. No. 69;
4; Mismatches 3; Indels
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Molecule type: mRNA
Residues: 1-1135 <CHI>
Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
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ate: 20-Sep-1999 #sequence_revisi
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Best Local Similarity 36.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                      Gene: T20D16.18; At2g23190
761-768, 1999
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A;Residues: 1-85 <PAR>
A;Crose-references: GB:AL513382; PIDN:CAD07537.1; PID:g16503529; GSPDB:GN00176
C;Genetics: A;Gene: parz
                                                                                                       56.1%; Score 37; DB 2; Length 85; 60.0%; Pred. No. 8.9;
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Matches 6, Conserv
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Q9ute7 schizosacch
P50466 escherichia
P14632 sus scrofe
Q41046 pinus sylve
Q24325 drosophila
Q24325 drosophila
P13368 drosophila
P14874 ascaris suu
P24874 ascaris suu
Q06399 salmonella
                            escherichia
sus scrofa
                                                                                       ascaris suu
escherichia
                                                pinus sylve
 chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Mammary gland; Cho Y.Y.; Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                   27-UL-1986 (Rel. 01, Created)
15-UL-1999 (Rel. 38, Last sequence update)
15-UN-1999 (Rel. 41, Last annotation update)
15-UN 2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A, Lactoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                                                           TISSUE=Mammary gland;
MEDLINE=90394839; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                       Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Mammary gland;
Liang O., Jimenz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
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Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                        TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; Q00756; Q9H1Z3; Q96KZ4;
Q9pjj9
P44693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Mammary gland;
Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]
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                                                                                                                                        ALIGNMENTS
        YEBA HAEIN
MSS1_SCHPO
AER ECOLI
TRFL PIG
TRFL PIG
TRFL PIG
TYDZ DROME
XPC DROME
7LES_DROME
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NULM ASCSU
YEDD ECOLI
YEDD SALTY
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475
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11211
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Submitted (MAY-1992)
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 P02788 homo sapien
Q9tum0 camelus dro
Q29477 capra hircu
P08071 mus musculu
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09xx18 drosophila
P93528 sorghum bic
P93789 salmonella
P41187 liberibacte
P49771 homo sapien
P12342 bos taurus
P26898 ovis aries
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vibrio chol
pseudomonas
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CHEZ PSEAE
VA16 VACCV
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TRFL_CAPHI
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DYHB_CHLRE
TRFL_HORSE
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PHYC_SORBI
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greo T., Tuochman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Blaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L., to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                             "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains."; Biochim. Biophys. Acta 670:243-254 (1981).
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PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE=82046817; PubMed=6794640; Jolles J., Spik G., Montreuil J.,
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 609-711.
MEDLINB-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 436-711 PROM N.A.
MEDLINE-88001031; Pubmed-3477300;
Rado T.A., Weil X., Benz E.J. Jr.;
"Isolation of lactoferrin CDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                            SECONDENCE OF 20'11.

MEDLINE-85076667; PubMed-6510420;

Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,

Legrand D., Spik G., Montreuil J., Jolles P.;

"Human lactotransferrin: amino acid sequence and structural
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253.-->methionine mutant.";
Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RÁY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
resolution."
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                TISSUE=Mammary gland;
MEDILINE=90326549;
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"Nucleotide sequence of human lactoferrin cDNA.";
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MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                               comparisons with other transferrins."
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Mol. Biol. 209:711-734(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91166929; PubMed=1369293; PubMed=1369293; PubMed=136929; PubMed=1369293; PubMed=1369293; PubMed=136929; PubMed=136929;
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
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-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
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                                                                                                              Acta Crystallogr. D 55:403-407(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF LACTOFERROXINS.
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SUBCELLULAR LOCATION: Secreted.
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M18642; AAA8665.1; -..
AF332168; AAG4873.1; -..
BC018822; AAH15822.1; -..
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EMBL, U07643; AAB60324.1; -.
EMBL, M93150; AAB36159.1; -.
EMBL, M83202; AAB59511.1; -.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
NCBL_TaxID=9925;
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Pred. No. 0.025;
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G -> A (IN REF. 2).

G -> P (IN REF. 2).

LLS -> PLF (IN REF. 2).

L -> F (IN REF. 2).

A -> P (IN REF. 2).

A -> Q (IN REF. 2).

A -> Q (IN REF. 2).

M, 0B0C175A0B69D430 CRC64;
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TISSUE=Mammary gland;
Ter T., Yu D.; Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 6 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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                                                                                                                                                               SIMILARITY.
SIMILARITY.
SIMILARITY.
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Best Local Similarity 75.0v
Lag 9, Conservative
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TRFL_CAPHI
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Tylopoda; Cameludae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=Somali, TISSUB=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ131674; CAB53387.1; -.
EMBL; AF166879; AAF82241.1; -.
EMBL; AF166879; AAF82241.1; -.
EMBL; AF166879; AAF82241.1; -.
EMBL; AF166879; TRANSFERIN.
EMINTS; PRO0425; TRANSFERRIN.
EMINTS; SMO0494; TRER, 2.
PROSTIE; PSO0206; TRANSFERRIN.1; 2.
PROSTIE; PSO0206; TRANSFERRIN.3; 2.
PROSTIE; PSO0206; TRANSFERRIN.3; 2.
EMOSTIE; PSO0207; TRANSFERRIN.3; 2.
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                             Length 711;
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LACTOTRANSFERRIN.
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55 BY SIMILARITY
192 BY SIMILARITY
192 BY SIMILARITY
194 BY SIMILAR
70 BY SIMIL BY
                          Score 64; DB 1; I
Pred. No. 0.00024;
0; Mismatches 1;
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     97.0%; Scc.
91.7%; Pred
                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                 1 CFOWORXMRKVR 12
                                                                                                                                                                                         39 CFOWORNMRKVR 50
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FISSUE-Uterus;
                       RESULT 4
TRFL MOUSE
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                                                                                                                         EMBL, U53857; AAA97558.1; --
EMBL, X7802; CAA5517.1; --
EMBL, X7802; CAA5517.1; --
INCEPPO, IPROOLISE, Transferrin.
Pfam, PF00405; transferrin; 2.
PRINTE; PR00424; TRANSFERRIN.
SMART; SM00042; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC...)
1 -> V (IN REF. 2).
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                         BY SIMILARITY.
LACTOTRANSFERRIN.
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Matches 8; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

Liu Z., Teng C.T.;

Liu Z., Teng C.T.;

Liu Z., Teng C.T.;

J. Biol. Chem. 266:21880-21885(1991).

J. Biol. Chem. 266:21880-21885(1991).

-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF PICARBONATE.

-! SUBUNIT: MONOWER.

-! SUBCLIULIAR LOCATION: Secreted.

-! DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

-! SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R WBL; J03299; AAA40525.1; --
R EMBL; D88510; BAA13633.1; --
R EMBL; D88510; BAA13633.1; --
R EMBL; M74778; AAA93427.1; --
R PIR; A28438; A28438
R HSSP; PO2788; LOS6.
R MGD; MGI:96837; Ltc
R Pfem; PRO0405; Lransferrin.
R Pfem; PRO0405; Lransferrin; 2.
R PROSITE; PS00205; TRANSFERRIN.
R PROSITE; PS00205; TRANSFERRIN.
R PROSITE; PS00207; TRANSFERRIN.
R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                          mouse
                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                        Pentecost B.T., Teng C.T.;
"Lactorransferrin is the major estrogen inducible protein of uterine secretions";
U. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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LACTOTRANSFERRIN.
1.
TREL MOUSE STANDARD; PRT; 707 AA. PREL MOUSE P08071, P70690; Q61799; Q922P2; Created) 1-AUG-1988 (Rel. 08, Created) PLUN-2002 (Rel. 41, Last sequence update) 15-UUN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                           IISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
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707
357
                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
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J. Cell Sci. 107:635-644(1994).
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
DYNEIN HAS ATTAKER ACTIVITY.
-!- SUBDINIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitchell D.R., Brown K.S., "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                    ANION (POTENTIAL).
ANION (POTENTIAL).
ANION (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> IQG (IN REF. 1).
R -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
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1-NOV-1997 (Rel. 35, Last sequence update)
30-MXY-2000 (Rel. 39, Last senotation update)
Dynein beta chain, flagellar outer arm.
DynA OR ODA-4 OR SUP1.
Chlamydomonas reinhardii.
Eukaryota, Viridiplantae, Chlorophyte, Chlorophyceae, Volvocales,
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S -> I (IN REF. 2).

A -> D (IN REF. 1).

L -> V (IN REF. 1).

L -> V (IN REF. 1).

F26AE0340A4C19A8 CRC64;
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MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 63.6%;
Matches 7; Conservative
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707 AA;
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-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBGNIT: MONOMER.
-!- SUBCRILIAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SUBCRILIAR LOCATION: TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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MICROTUBLIABLE SINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                              EMBL, U02963, AAA19956.1; -. Interpro; IPR04273; Dynein heavy.
Pfam; PP03028; Dynein heavy, 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65.2%; Score 43; DB 1; Length 4568; 50.0%; Pred. No. 11; 3; Indels cive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09 ATP (POTENTIAL).
37 ATP (POTENTIAL).
36 ATP (POTENTIAL).
519961 MW; 9A9A5393C7C36AE7 CRC64;
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AA
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30-MAY-2000 (Rel. 39, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update)

Nebula protein. NLA OR CG6072.

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                                                                                                                                                                                                                                Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Signal; 3D-structure.

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SIGNAL <1 6
CHAIN 7 695 LACTOTRANSFERRIN.

REPEAT 7 350 1.
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Pred. No. 9.3;
3; Migmatches 2; Indels
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IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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PDB, 1BTV, 02-DEC-98.
PDB, 1BTV, 02-PEB-99.
PDB, 1BTV 02-PEB-99.
INTER-PRO, 1PR001156; Transferrin.
Pfam, PP00405; transferrin, 2.
PRINTS, SM00094; TR FER, 2.
PROSITE; PS002056; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                        EMBL; AJ010930; CAA09407.1; -.
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Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                         STRAINBERKELE, NOT AND AGE 10731132; AGENCAME C.A., GOCCATHE J.D., VAR MEDLINESCREECH S.E., Holt R.A., Evans C.A., GOCCATHE J.D., VAR MEDLINESCREECH S.E., Holt R.A., Evans C.A., GOCCATHE Y.D., Celliker S.E., Holt R.A., Evans C.A., GOCCATHE Y.N., Henderson S.N., GOCCOG G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., As Barndon R.C., Rogers Y.-H.C., Blazel R.G., Change M., Peffifer B.D., Wan X.H., Doyle C., Bardenia A., An H.-J., Andrews-Pérantoch C., Baldwin D., Ballew R.M., Beau A., Barndon R.R., Miklos G.L.G., Wand R.R., Caller R.G., Helt G., Walson C.R., Miklos G.L.G., Baldwin D., Ballew R.M., Caller B., Burtler H., Cadieu E., Center A. Chandra I., Bartler R.C., Busam D.A., Butler H., Cadieu E., Center A. Chandra I., Bartler K.D., Caller B., Downes M., Deng Z., Mays A.D., Dew I., Diez S.M., Ge Pablos B., Deldcher A., Deng Z., Mays A.D., Dew II., Diez S.M., Andrew J. Burtles R.C., Dunn P., Domen K.J., Evangelista C.C., Ferrac C., Ferriera S., Dinkow B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Dischman W., Andrew B. D., Dew II., Diez S.M., Deng Z., Gann P., Harris M., Houck Y., March D., Dew II., Houck Y., March D., Dew II., March M., Golde R., McIntoeh T.C., Meinel D., Harris M., Jalali M., Kalush P., Kardt C., Kervitz S., Kulp D., Lai Z., Lias Y., Lei Y., Morsh K., Mosher D., Jala J., March D., Dill, J., Lid, J., Lid,
                                                       Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                               Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF147700; AAD33987.1; -.
EMBL; A8003712; AAF55285.1; -.
FlyBase; FBGM0026629; nla
SEQUENCE 292 AA; 31423 WW; 64F1BBF5F6EA6CF9 CRC64;
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292 AA

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NLA DROME STANDARD; Q9XZLB; Q9V391; 30-MAY-2000 (Rel. 39, Created)

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RESULT 7 NLA DROME

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us-09-743-107b-89.rsp

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PMRD SALTY
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                                                                                                                                                                                                                 Sorghum bicolor (Sorghum) (Sorghum vulgare),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
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                              Gaps
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-1- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-1- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-1- SIMILARITY: CONTAINS 2 PAS (PEE-ARNT-SIM) DIMERIZATION DOMAINS.
-1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                           MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                               .;
0
 57.6%; Score 38; DB 1; Length 292; 54.5%; Pred. No. 6; ive 2; Mismatches 3; Indels
                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                    1135 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; US6731; AAB41399.1; InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003104; GAR.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR004361; His_Kinh.
InterPro; IPR004610; PAG.
InterPro; IPR000014; PAG.
InterPro; IPR001294; PHytochrome.
Pfam; PF00360; phytochrome; I.
Pfam; PF00369; PAS, 2.
Pfam; PF00319; PAS, 2.
Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MECLINE=21534948; PubMed=11677609;
MCCI-elland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multiple family. PAS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94266712; PubMed=8206837;
Acland K.L., Bether C.R., Spitznagel J.K.; mit. from Salmonella "Isolation and characterization of a gene, pmrD, from Salmonella typhimurium that confers resistance to polymyxin when expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
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Pred. No. 23;
4; Mismatches 3; Indels
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1135 AA, 126315 MW, AFCC934B7592DB4D CRC64,
                                                                                                                                                                                                                                                                                                                                                                                         PAS 2.
HISTIDINE KINASE.
SMART; SM00387; HATPASSEC; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRFAMS; TIGR00229; SENSORY, DOX; 2.
PROSITE; PSS0109; HIS KIN; 1.
PROSITE; PSS0112; PAS; 2.
PROSITE; PS00245; PHYTOCHROME 1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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J. Bacteriol. 176:3589-3597(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.6%;
36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U02281; AAA21322.1; -.
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1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "FRAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=20343011; PubMed=10881197;
Savvides S.N., Booner T., Karplus P.A.;
Savvides S.N., Booner T., Tarplus P.A.;
"Flt3 ligand structure and unexpected commonalities of helical
bundles and cystine knots.";
Nat. Struct. Biol. 7:486-491(2000).
Nat. Struct. Biol. 7:486-491(2000).
-i. FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOLETIC
CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       secreted (isoform 2).
-!- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR004213; Flt3_lig.
Pfam; PP02947; flt3_lig; 1.
Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-942358642; PubMed-8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.D., James L., Johnson L., Brasel K., de Vries P., Bscobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells."; Blood 83:2795-2801(1994).
                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
ligand) (Flt31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91195428; PubMed=8145851;

MEDLINE=91195428; PubMed=8145851;

Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,

Hannum C., Mattson J., Luh J.,

Bazan J.F., Kaselelin R., Hudak S., Wagner J., Mattson J., Luh J.,

Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,

Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,

Zlornik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;

Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of

haematopoietic stem cells and is encoded by variant RNAs.";

Nature 368:643-648 (1994).
                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FACTORS AND INTERLEUKINS.
-!- SUBUNIT: Homodimer (isoform 2).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
235 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U04806; AAA17999.1; -. EMBL; U03859; AAA19825.1; -. EMBL; U29874; AAA90949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29874; AAA90950.1; -.
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STANDARD;
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   WWW WE WANTED THE WARKEN WAS A COUNTY OF THE WARKEN WAS AND THE WAS AND THE WAS A COUNTY OF THE WAS A COUN
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Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Planet P., Jagoueix S., Bove J.M., Garnier M., Itrus Greening "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (RC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate {RNA} (N).
-!- SUBDWIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA' CHAIN.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                   Score 37; DB 1; Length 85; Pred, No. 2.7;
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Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BTA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
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   EMBL; AE008803; AAL21205.1; -
Stydene; SG10384; pmrD.
Antibioria resistance; Complete proteome.
SEQUENCE 85 AA; 9749 MW; 1E1922419EA50CCA CRC64;
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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SEQUENCE 146 AA;
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Best Local Similarity
Matches 6; Conserv
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ID RPOB_LIBAF
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POTENTIAL

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PSOURCE OF 1-21 FROM N.A.

PSOURCE OF 1-21 FROM N.A.

A YOO J., de Leon F.A., Stone R.T., Beattie C.W.;

T "Cloning and chromosomal assignment of the bovine interleukin-2

T receptor alpha (IL-2R alpha) gene.";

Mamm. Genome 6:751-753(1995).

C -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.

C -!- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

EXIST IN 3 DIFFERENT FORMS: A HIGH APPINITY MONOMER (ALPHA

C CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE

MITH A GAMMA CHAIN.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the butopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch.
                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
DSSTLPPPWSPREATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
G -> A (IN REF. 1).
73895BF693B4CECF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88212503; PubMed=2835311; Meinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S., Reeves R., Magnuson J.A.; Revers R., Magnuson J.A.; "Cloning of CDNA for the bovine IL-2 receptor (bovine Tac antigen)."; Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2010 (Rel. 40, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 1; Length 235;
Pred, No. 11;
                       SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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N-LINKED
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
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235 AA;
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P12342;
                                              DOMAIN
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DISULFID
DISULFID
CARBOHYD
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01-AUG-1992 (Rel. 23, Last sequence update)
01-RB-1996 (Rel. 33, Last anottation update)
Interlebkin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
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Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
11.1.
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BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLOCHAC. .) (POTENTIAL).

N-LINKED (GLOCHAC. .) (POTENTIAL).
                                                                                                                                                           INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
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0
                                                                                                            Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi. SIGNAL 1 2 2 275 INTERLEUKIN-2 RECEPTOR ALPHA CHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 1; Length 275;
Pred. No. 13;
1; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   4901BBF9A4862390 CRC64;
                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
PIR; S07442; S07442.
HSSP; P01589; 11LM.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PP00084; sushi; 2.
SWART; SM00032; CCP; 2.
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Best Local Similarity 50.ve,
G; Conservative
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22643
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CARBOHYD
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ATX1_ARATH
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ARE REVERSHELY INTERCONVERTIBLE BY LIGHT. THE PR FORM THAT ABSORBS

ARE REVERSHELY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS

MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PER CONTROLS THE SPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Nipponbare,
Tahir M., Kanegae H., Takano M.;
Tahir M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of
a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 275-378 FROM N.A.
MEDLINE=97019052; PubMed=886568;
MATHEWS A., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and "The phytochrome gene family in grasses and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINYED (GLCHAC. . .) (POTENTIAL).
S -> T (IN REF. 2).
W, 1101A2DB5AC5A088 CRC64;
                                                                                                                                                                                                                                                                          Receptor; Repeat; Signal; Sushi.
BY SINILIARITY.
INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%; Score 36; DB 1; Length 275; 50.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL) SUSHI 1. SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHYCORYSA STANDARD; PRT; 1137 AA. 092MT9; pp. 993429; pp. 002CT-2001 (Rel. 40, Last sequence update) pp. 16-0CT-2001 (Rel. 40, Last sequence update) pp. 15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                   EMBL; 211560; CAA77652.1; --
EMBL; X60149; CAA4723.1; --
EMBL; X60149; CAA01447.1; --
PIR; S18910; S18910.
PIR; S18999; PIR; JG113; JG113; JG113; JG1113; JG11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30904 MW;
                                                                                                                                                                                                                                                                            Transmembrane, Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 50.0 nes 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 CLIWQRRWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 1
152 1
80
166 1
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytochrome C. PHYC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiosperms.";
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TRANSMEM
DOMAIN
DOMAIN
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CONFLICT
SEQUENCE
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DISULFID
DISULFID
DISULFID
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PHYC_ORYSA
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BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE! () IN A NEGATIVE FEEDBACK PASHION.
-!- SUBJUNT: HOWODIMER (BY SIMILARITY).
-!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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16-0cr-2001 (Rel. 40, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Potential cation-transporting ATPase (BC 3.6.3.-).
Argazasa OR MQMI.11.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TICRFAMS; TICR00229; sensory box; 2.
PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PS00245; PAS; 2.
PROSITE; PS00245; PAYTOCHROWE 1; 1.
PROSITE; PSS0046; PHYTOCHROWE 2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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Pred. No. 54;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F -> S (IN REF. 2).
C -> S (IN REF. 2).
My, F2A520181CFE7B32 CRC64;
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EF. 2).
EF. 2).
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PAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY S)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB018442; BAA74448.1; -...
EMBL; U61207; AAR41996.1; -...
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003151; Has InterPro; IPR003151; Has KIN sig. InterPro; IPR003661; His KIN sig. InterPro; IPR003661; His KIN sig. InterPro; IPR001610; PAS. InterPro; IPR001294; Phytochrome: Pfam; PR00360; phytochrome; 1. Pfam; PR00360; phytochrome; 1. Pfam; PR00360; phytochrome; 1. Pfam; PR003512; signal; 1. Pfam; PR003518; Harbase c; 1. Pfam; PR01033; PHYTOCHROME. SWART; SM00365; GAF; 1. SWART; SM00365; GAF; 1. SWART; SM00365; Harbase c; 1. SWART; SM00366; PAS; 1. SWART; SM00366; PAS; 2. SWART; SM00366; PAS; 2. SWART; SM003691; PAS; 2. SWART; SM00361; PAS; 2. SWART; SM00391; PAS; 2. SWART; 2. SWART; SM00391; PAS; 2. SWART; SM00391; PAS; 2. SWART; 2. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match
Local Similarity 36.4%;
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125982
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279 27
292 29
1137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 CLEWNEAMOKI 787
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                                                                                                                                                                                                                                        Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence seatures of the regions of 3,076,755 bp covered by sixty P1 and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RINTS; PR00119; CATATPASE.
ROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Saro S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                   Closs.";

DNA Res. 7:31-63(2000).

-!- PUNCTION: INVOLVED IN TRANSPORT OF CATIONS (POTENTIAL).

-!- CATALYTICA CATIVITY: ATP + H(2)O = ADP + phosphate.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBPAMILY V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Pred. No. 56;
3; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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InterPro; IPR001757; ATPase B1-E2.
InterPro; IPR001454; Hignase/hydriase.
Pfan; PF00122; B1-E2 ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491
812
816
NA: 131115 MW:
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Best Local Similarity 44.4%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                034
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1179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lagnesium.
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FRANSMEM
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TRANSMEM
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SEQUENCE
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Gaps

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1 CFQWQRXMR 9

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1144 CYSWERLLR 1152
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Search completed: February 21, 2003, 07:51:37 Job time : 6.2093 secs

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Q99ws6 lycopersico
Q98x56 salmonella
Q9ygCo human immun
Q9ygCo human immun
Q9ygBo human immun
Q9yj17 human immun
Q9yj17 human immun
Q9yj17 human immun
Q9yj17 human immun
Q9yl16 human immun
Q8G454 human immun
Q8G454 human immun
Q8G454 human immun
Q8G454 human immun
Q8HA3 caenorhabdi
Q91xw0 homo sapien
Q91xw0 homo sapien
Q91xw1 homo sapien
Q91xw3 homo sapien
Q91xw3 homo sapien
Q91xy3 hala rabaldopsis
Q9hm3 halabacteri
Q9by37 homo sapien
Q8srg1 encephalito
Q8srg1 encephalito
Q8srg1 encephalito
Q9srg1 lumpy skin
Q95hig arabidopsis
Q9fhig arabidopsis
Q9fhig arabidopsis
                                                           O22185 arabidopsis
O22188 arabidopsis
096m21 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 'Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-TMN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human) (Fragment).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.4%; Score 59; DB 4; Length 711; 90.9%; Pred. No. 0.0067; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBTCD2;
01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
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Q9ZTP0
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            Best Local Similarity 90.9
Matches 10; Conservative
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TISSUE=PROSTATE;
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Q9tcd2 homo sapien
Q9tr80 ovtsa saties
Q9xt86 ovtsa satie
Q9xt85 ovtsa satie
Q9x191 sesamum ind
Q91780 caenorhabdi
Q9153 caenorhabdi
Q9163 arnochabdi
Q8062 arnochabdi
Q9x18 rhizobium i
Q9x18 rhizobium m
Q8xe2 ralstonia s
Q8xe2 ralstonia s
Q8xe2 homo sapien
Q97855 human immun
Q77855 human immun
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114.078 Million cell updates/sec
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                                                                                                                                                                                                           February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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                                  GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Maximum Match 1008
Listing first 45 summaries
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Q9UCY5
Q9TR80
Q9XFD5
Q9XFD1
Q93FD3
Q9BCA2
Q9BCA2
Q9ZRH8
Q8XFX3
Q8XFX3
Q8XFX3
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Q9TXX2
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Q9TXX2
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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66
1 CFGWQRXMRKVR 12
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STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Mu L.S.H., Chen E.C.F., Tzen J.T.C.;
"Molecular cloning of 118 globulin and 28 albumin, the two major seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryora; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sesamum indicum (Oriental sesame) (Gingelly).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids i; Lamiales; Pedaliaceae; Sesamum.
genes that are differentially expressed at rice young panicle."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AR140486; AAD29699.1; -.
InterPro; IPRO01128; Cytochrome_P450.
FRINTS; PRO0067; P450.1
PRINTS; PRO0185; P450.
PROSITE; P800086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenage; Oxidoreductase.
NON_TER.
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                                                                                                                                                                                                                  Query Match 62.1%; Score 41; DB 10; Length 105; Best Local Similarity 60.0%; Pred. No. 2.3; Matches 6; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                storage proteins in sesame.";
J. Apric. Food Chem. 47:4932-4938 (1999).
EMBL; AF091841; AAA42943.1;
InterPro; IPR001612; AAI.
InterPro; IPR00168; TV Mpin.
InterPro; IPR00168; TV Mpin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00499; AAI: 1.
SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                     SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02,
01-AUG-1998 (TrEMBLrel. 07,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Caenorhabditis elegans.
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                            1 CFQWQRXMRK 10
                                                                                                                                                                                                                                                                                                               61 CPQWERLGKK 70
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Q93780;
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01-NOV-1999 (TrENBLrel. 12, Last sequence update)
01-MAR-2002 (TrENBLrel. 20, Last annotation update)
Cytochrome P450 (Fragment).
Cytoza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Bovidae, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,

Bovidae, Caprinae, Ovis.
                                                                                                   Sato I., "Characterization of the 84-kDa protein with ABH activity in human
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TISSUB=PANICLE,
Liu J., Yang J.,
"Suppression subtractive hybridization (SSH) identified candidate
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                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.8%; Score 50; DB 6; Length 33; llarity 63.6%; Pred. No. 0.014; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                         83.3%; Score 55; DB 4; Length 38; 90.9%; Pred. No. 0.0019; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.

MEDIINE=55127729; PubMed=7827104;

MEDIINE=55127729; PubMed=7827104;

Biochim. Biophys. Acta 1243:25-32 (1995).

HSSP: 077698; ICE2.

HTGSPPO 777698; Transferrin.

Pfam; PG00405; transferrin; 1.

SEQUENCE 33 AA; 3914 MW; D1904CABISA73961 CRC64;
                                                                                                                                                                                       InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                       seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                                SEQUENCE FROM N.A. MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRXMRKV 11
                                                                                                                                                                                                                                                                                                                                2 FOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                 21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 10; Conserv
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les 7; Conser
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                                                                                                                                                                                                                                                           Query Match
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Matches
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                  SON TENENT TENENT SON
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none;

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Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21608569; PubMed=11743193; Monks D.E., Kitajima J.P., ModLINE=21608569; PubMed=11743193; Monks D.E., Kitajima J.P., Mood D.W., Setubal J.C., Kaul R., Monks D.E., Almeida N.F. Jr., Woo L., Chen Y., Zhou Y., Chen L., Mood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendening J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Kreepan W., Perry M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
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                                                                                                                                                                                Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxamine 5-phosphate oxidase.

PDXH OR ATU0760 OR AGR C 1381.

Agrobacterium tumefaciens (strain C58 / ATCC 33970).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 16; Length 205;
Pred. No. 11;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBUHC2;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 7:331-338(2000).

BMBL, ADO03011, RAB53533.1; -.

InterPro, 1PR000659; Pyridox oxidase.

Pfam, PF01243; Pyridox oxidase; 1.

ProDom, PD006312; Pyridox oxidase; 1.

IIGRNS; TIGR0558; paxH; 1.

PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21082930; PubMed=11214968;
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MEDLINE=21608551; PubMed=11743194;
                                                                                                                                    Pyridoxamine 5'-phosphate oxidase.
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PRELIMINARY;
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Best Local Similarity
Matches 6; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRXMRKVR 12
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QBUHC2
DDT TO COCCOS OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ક
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for investigating biology."; cience 282:2012-2018(1998).
EMBL; Z81089; CARB0317:1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       60.6%; Score 40; DB 5; Length 275; 63.6%; Pred. No. 9.7; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.6%; Score 40; DB 5; Length 932; 63.6%; Pred. No. 34; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Waterston R.;
"Direct Submission.";
Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U50308; AAG24025.1; -.
                                                                  Dobson 8.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Favello A., Gatung S.;
"The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            al protein.
932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q19153;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 AA
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PROSITE; PS50156; SSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.0-
Per 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 FOWKISMRKTR 272
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                      SEQUENCE FROM N.A.
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SEQUENCE 93
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Query Match

Best Loca Matches

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Gaps

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us-09-743-107b-89.rspt

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SEQUENCE FROM N.A.

STAIN=16M / ATCC 24456 / BIOTYPE 1;
STRAIN=16M / ATCC 24456 / BIOTYPE 1;
STRAIN=16M / ATCC 24456 / BIOTYPE 1;
AMEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
All Janova N., Anderson I., Bhattacharrya A., Lykidis A., Rezzik G.,
Anderson I., Bhattacharrya A., Lykidis A., Rezzik G.,
Anderson I., Bhattacharrya A., Lykidis A., Mazur M., Golteman E.,
Anderson I., Larsen N., D'Souza M., Bernal A., Mazur M., Golteman E.,
Anderskorn R., Kyrpides N., Overbeek R.;
Anderskorn R., Kyrpides N., Overbeek R.;
Are genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
Procon Natl. Acad. Sci. U.S.A. 99:443-448(2002).
REMBL; ARO09587; AALS5698.1; -.
RemBL; ARO09587; AALS5698.1; -.
RemBL; ARO09587; AALS5698.1; -.
RemBL; ARO09587; Pyridox_oxidase.;
RemBL; ARO00512; Pyridox_oxidase.;
Recomplete Prince Procone.

Coxidoreductase; Complete proteome.

Coxidoreductase; Complete proteome.

SQUENCE 208 AA; 23866 MW; CBIF50BC9612DE28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salahoubat M., Genin S., Artignenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguler P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid megaplasmid.
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.1%; Score 39; DB 16; Length 208; 50.0%; Pred. No. 11; 4; Indels ive 2; Mismatches 4; Indels
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       01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (BC 1.4.3.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31541 MW; ABB38818004B2EDA CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas solanacearum)
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InterPro, IPR004843; M-ppestrase.
InterPro, IPR004844; S/T phosphtse.
Pfam, PF00149; Metallophos; 1.
Plasmid, Complete proteome.
SEQUENCE 279 AA; 31541 MW; ABB38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 CFHWKSLRROVR 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQRXMRKVR 12
                                                                                                          Brucella melitensis.
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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Q8XSE2
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Hountel K., Gordon J., Vaudin M., Tartchouk O., Epp. A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Gielo C., Slater S., Strub G., Agrobacterium tumefaciens C58."; Science 294:3232-3238(2001).

EMBL, ABC09043; AAL4176-1; -.

EMBL, ABC08009; AAK86569:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLOWER TO SMC00069.

PDXH OR R00895 OR SMC00069.

Rhizobium meliloti (Ginorhizobium meliloti).

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Pred. No. 11; 4; Indels
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.1%; Score 39; DB 16; Length 206; ilarity 50.0%; Pred. No. 11; Conservative 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
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(TrEMBLrel. 20, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21396507; PubMed=11481430;
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SEQUENCE FROM N.A.
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01-MAR-2002
01-MAR-2002
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SOW KWA KRANA KRAN

Q92RH8 **Q92RH8** 

RESULT 10 Q92RHB

Best Loca Matches

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OBYFK3

RESULT 11 QBYFK3

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1 CFOWORXMRKVR 12

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TISSURE-PLACENTA;

A ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Magai K., Sugano S., Shirarori A., Sudo H.,

Nishikawa T., Magai T., Kawu Y., Kodaira H., Kondo H., Sugawara M.,

A Wagateuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

A Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

A Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

A Ninomiya K., Twayanagi T.,

INEDO human cDNA sequencing project.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AKO02037; BAA92048-1;

INTERPRO, IPRO00008; C2.

R InterPro; IPRO00504; RNA_rec_mot.
                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ1175.
Bukaryoca, Merazo; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FL011175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacy1gycerol-binding protein UNC-13.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1; -.
Hypothetical protein: SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
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SMART; SMO0369; C220MAIN.

PROSITE; PS00499; C2 DOWAIN. 1; UNKNOWN_1.

PROSITE; PS50004; C2 DOMAIN. 2; 1.

PROSITE; PS500009; REM RNP 1; UNKNOWN 1.

SEQUENCE 466 AA; 53192 MW; E4113Ã5062F58D6E CRC64;
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Best Local Similarity 55.6.
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244 CFOWEKGTRIAK 255
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TISSUE=PANCREAS;
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                                                                                       ESULT 13
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EMBL, 247867; CAA87881.1; -. InterProy; IRRON0777; GP120.

Fam: PF00516; GP120.

Pfam: PF00516; GP120.

ALDS; Coat protein; Glycoprotein.
Query Match
59.1%; Score 39; DB 4; Length 466;
Best Local Similarity 55.6%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 2; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus.
VOZI_TaxID=11676;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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1 1 1 2 2 17 AAR87651 5 4 97.0 20 17 AAR87651 5 6 4 97.0 20 17 AAR87652 5 6 4 97.0 20 17 AAR87652 5 6 97.0 20 17 AAR87652  AAIGNMENTS  T 1 AAY78074 standard; Peptide; 12 AA. AAY78074;  25-APR-2000 (first entry)  Human lactoferrin derived peptide SEQ ID NO:74.  Human lactoferrin; modification; infection; inflammat trans, lactoferrin; auti-inflammatory; anti-microbia urinary tract infection; colitis; Candida infection; fordinary tract infection; colitis; Synthetic.  MOZO0001730-A1.  13-JAN-2000.  15-JUL-1998; 98SE-0002662.  29-DEC-1998; 98SE-0004614.  AASCI-) A+ SCI INVEST AB.	11   64   97.0   14   21   AAY78036   Human   actoferrin     13   64   97.0   14   21   AAY78036   Human   actoferrin     14   64   97.0   15   21   AAY78035   Human   actoferrin     15   64   97.0   15   21   AAY78035   Human   actoferrin     16   64   97.0   15   21   AAY78035   Human   actoferrin     18   64   97.0   15   21   AAY78035   Human   actoferrin     19   64   97.0   16   21   AAY78031   Human   actoferrin     20   64   97.0   16   21   AAY78031   Human   actoferrin     21   64   97.0   16   21   AAY78034   Human   actoferrin     22   64   97.0   17   21   AAY78034   Human   actoferrin     24   64   97.0   17   21   AAY78035   Human   actoferrin     25   64   97.0   18   17   AAY8034   Human   actoferrin     26   64   97.0   18   17   AAY78035   Human   actoferrin     27   64   97.0   19   21   AAY78035   Advanced glycosyla     28   64   97.0   20   18   AAX8839     29   64   97.0   20   18   AAX8830     20   20   20   3   AAX8830     20   20   3   AAX8830     21   34   64   97.0   20   15   AAX88056     31   64   97.0   20   15   AAX88056     32   64   97.0   20   16   AAX88056     33   64   97.0   20   16   AAX88056     34   64   97.0   20   16   AAX88056     35   64   97.0   20   16   AAX88056     36   64   97.0   20   16   AAX88056     37   84   97.0   20   16   AAX88056     38   64   97.0   20   17   AAX89057     40   64   97.0   20   17   AAX89057     41   64   97.0   20   17   AAX89057     42   64   97.0   20   17   AAX89057     44   64   97.0   20   17   AAX89057     45   64   97.0   20   17   AAX89057     46   97.0   20   17   AAX89057     47   64   97.0   20   17   AAX89057     48   64   97.0   20   17   AAX89057     49   64   97.0   20   17   AAX89057     40   64   97.0   20   17   AAX89057     41   64   97.0   20   17   AAX89057     42   64   97.0   20   17   AAX89057     44   64   97.0   20   17   AAX89057     45   64   97.0   20   17   AAX89057     46   97.0   20   17   AAX89057     47   64   97.0   20   17   AAX89057     48   64   97.0   20   17   AAX89057     49   64   97.0   20
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicial and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                         Claim 22; Page 35; 102pp; English.
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91.7%;
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98SE-0004614.
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Best Local Similarity 91...
Lines 11; Conservative
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29-DEC-1998;
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AAY78038
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 7.9e-05;
0; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                      97.0%; Score 64; DB 21; Length 12; 91.7%; Pred. No. 7.9e-05; ive 0; Mismatches 1; Indels
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Matches 11; Conserv
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lactoferin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment urinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

AAY78001 to AAY78100 represent peptides having sequences based on human

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through the intestine transported binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unbrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used also because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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llarity 91.7%; Pred. No. 7.9e-05;
Conservative 0; Mismatches 1; Indels
                                                       Score 64; DB 21; Length 12;
Pred. No. 7.9e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:86.
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                                                                                                                                                                                                                                                                                                                                                                                                     AAY78086 standard; Peptide; 12
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98SE-0002562.
98SE-0004614.
                                                          97.0%;
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Conservative
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Best Local Similarity
Matches 11; Conserv
                                                                                           Similarity
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29-DEC-1998;
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Matches 11;
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Sequence
                                                          Query Match
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AAY 78086

AAY 7808

AAY 78
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(first entry)

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Human, lactoferrin; modification, infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                            Human lactoferrin derived peptide SEQ ID NO:90.
AAY78090 standard; Peptide; 12 AA.
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29-DEC-1998;
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                                    AAY78090;
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  AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as urinary tract inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also function though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used as used as because of high production costs. Therefore, provision of peptides based on lactoferrin would contable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                 Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour;
urinary tract infection, colitis, Candida infection, fungicidal;
bactericidal, preservative.
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                                                                                                                                    AAY78089 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                    1 CFÓWÓREMRKVR 12
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    1 CFOWORXMRKUR
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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Dolphin GT;

Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

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AAY78001 to AAY78100 represent peptides having sequences based on human lacocferrin. The peptides are taken up in the intestine through the inding to specific lactoferrin receptors and are then transported binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal mebrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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es 12; Conserv
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97.0%; Score 64; DB 21; Length 12; 100.0%; Pred. No. 7.9e-05; ive 0; Mismatches 0; Indels

Query Match Best Local Similarity 100. Matches 12; Conservative

CFQWQRXMRKVR 12 1 CFOWORXMRKVR 12

RESULT 7

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Seven though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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98SE-0002562.
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Best Local Similarity
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Dolphin GT;

Baltzer L,

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as unimary tract infections and/or tumours. The peptides can also be used membrane), inflammations and/or tumours. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides they cannot be used as breasted anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 8.6e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                            Dolphin GT
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98SE-0002562.
98SE-0004614.
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91.7%;
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Best Local Similarity 91.7
Matches 11, Conservative
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 Synthetic.
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Score 64; DB 21; Length 13; Pred. No. 8.6e-05; 0; Mismatches 1; Indels

97.0%;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on mucossal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64; DB 21; Length 13; Pred. No. 8.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                    Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78036 standard; Peptide; 14 AA.
                                                                                                           Mattsby-Baltzer I,
             98SE-0002441.
98SE-0002562.
98SE-0004614.
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91.7%;
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98SE-0004614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal, preservative
                                                                          (ASCI-) A+ SCI INVEST AB.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
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17-JUL-1998;
29-DEC-1998;
           06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unihary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-miorobial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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                                                              New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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Baltzer L,
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                                                                                                               Claim 12, Page 69; 102pp; English
Mattsby-Baltzer I,
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98SE-0004614.
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                                WPI; 2000-147388/13.
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ses 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         14 AA;
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17-JUL-1998;
29-DEC-1998;
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Hanson LA,
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Matches
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colitis, and Candida infection on
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                 14 AA;
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                              AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food sutiffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumo
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                     Score 64; DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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Claim 15; Page 75; 102pp; English.
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Best Local Similarity 91.7
Matches 11; Conservative
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17-JUL-1998;
29-DEC-1998;
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membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have deelred anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 21; Length 14;
Pred. No. 9.2e-05;
0; Mismatches 1; Indels
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Pred. No. 9.8e-05;
0; Mismatches 1; Indels
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AAY78035
ID AAY78
XX
AC AAY78
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DT 25-APR-2000 (first entry)
XX
DE Human lactoferrin derived peptide SEQ ID NO:35.
XX
W Human; lactoferrin; modification; inflammation; tumour;
XW food; infant formula; anti-inflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory; anti-inflammatory;
XX
Homo sapiens.
Synthetic.
XX
WO200001730-Al.
XX
PD 13-JAN-2000.
XX
PD 13-JAN-2000.
XX
PC-JUL-1999; 9980E-0002441.
PR 17-JUL-1998; 988E-0002562.
PR 29-DEC-1998; 988E-0002562.
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Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin

(ASCI-) A+ SCI INVEST AB.

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 69; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urhary tract infections, colltis, and Candida infection on a mucosal membrane). Inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cost.

Sequence 15 AA;

Query Match
97.0%; Score 64; DB 21; Length 15;
Best Local Similarity 91.7%; Pred. No. 9.8e-05;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps

1 CFQWQRXMRKVR 12

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Search completed: February 21, 2003, 07:56:43 Job time : 28.093 secs

4 CFQWQRNMRKVR 15

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3, Application US/08204487
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STRANDEDNESS: si
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STATE: MA
COUNTRY: USA
ZIP: 02109
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Sequence 3,
Patent No.
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                                                    February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3,
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Sequence 2
Sequence 2
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Sequence 4
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/ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
/ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
/ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
/ggn2_6/ptodata/1/iaa/RGTUS_COMB.pep:*
/ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-204-487.1
US-08-256-771-24
US-08-381-984-24
US-08-381-984-24
US-09-508-734-4
US-09-508-734-6
US-07-755-161A-10
US-07-981-74-10
US-07-981-74-10
US-08-608-734-8
US-08-508-734-8
US-08-508-734-8
US-08-508-734-8
                                                                                                                                                             Potal number of hits satisfying chosen parameters:
                                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     OM protein - protein search, using sw model
                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                       Issued Patents AA:*
                                                                                    US-09-743-107B-90
66
                                                                                                                                                                              Winimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                      1 CFQWQRXMRKVR 12
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Match Length
                                                                                      Fitle:
Perfect score:
                                                                                                                     Scoring table:
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                                                                                                      Sequence:
                                                                                                                                              Searched:
                                                      Run on:
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No.
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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATRAU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: TKWASAKI, YOSHIHIRO
APPLICANT: TKWASAKI, YOSHIHIRO
APPLICANT: INTERO FINUENTION: INTERITORS
NUMBER OF ENQUENCES: 8
CORRESPONDENCE ADDERSS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
GITY: MASTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
FRATURE:
NAMBKEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIP: 02109
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT ARPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFTATEN NUMBER: 134
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL; PAULA:
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELEFRATION INFORMATION:
TELEFRAX: (617) 248-700
INFORMATION FOR EGO ID NO: 3:
SEQUENCE CHRACTERISTICS:
LENGTH: 18 amino acids
WOLD TELEFACTURE INFORMATION:
SEQUENCE CHRACTERISTICS:
LENGTH: 18 amino acids
                                      US-08-724-586-2
US-09-921-632-2
US-08-655-640-2
US-08-655-640-4
US-08-461-333-4
US-08-461-333-4
US-08-461-333-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-456-106-2
US-08-456-108-2
US-08-456-108-2
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US-08-456-108-2
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TELEX: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08485948

Patent No. 5855882

GENERAL INFORMATION:

APPLICANT: YONG MING LI

APPLICANT: ANTHONY CREAMI

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: BIDPRODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS: 9

CORRESPONDENCE ADDRESS: 9

CONRESPONDENCE ADDRESS: 9

COMPUTER: New Jersey

COMPUTER: New Jersey

COMPUTER: BADABLE FORM:

MEDIUM TYPES: Floppy disk

COMPUTER: BADABLE FORM:

MEDIUM TYPES: PLODS/MS-DOS

SOFTWARE: BATCHIN Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/485,948

FILIGO ADDRESS: ADDRESS: PLOSTEN: ADDRESS:
                                                                                                                                                                              Gaps
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                                                                                                          Length 18;
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Pred. No. 3.8e-05
0; Mismatches
                                                                                                      97.0%; Score 64; DB 1;
91.7%; Pred. No. 3.8e-05
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
PRIOR APPLICATION DATA:
FILING DATE: 08/486,217
FILING DATE: UNNER: 08/486,217
FILING DATE: DATE: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESG., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-07
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE: 201 487-5800
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.0%;
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEO ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                      Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                              1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                               1 CFOWORNMRKVR 12
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TELEX: 13
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CFOWORNMRKVR 12

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Sequence 6, periodication US/08c20300

Sequence 7, periodication US/08c20300

Sequence 8, periodication US/08c20300

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LOCATION: 19
IDBNIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRATURE:
NAME/KEY: modified site
LOCATION: 2
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%; Score 64; DB 1; Length 20;
                                                                       US/07/755,161A
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FILING DATE:
PRILOND DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                          SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NOATS:
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek Jr.,
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
       OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
ITYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUR TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
INMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-755-161A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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       CORRESPONDENCE ALL ALLAGESON
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STATE: 07601

COUNTRY: USA

ZITE: 07601

COMPUTER ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE: 08/488,217
FILING DATE: 08/488,217
FILING DATE: 1995
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/48,42
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 26,742
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 26,742
FILING DATE: 487-5800
TELEFRAL 201 343-1684
TELEFRAL 18 amino acids
TVPR: amino acids
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Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: 0.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 64; DB;
Pred. No. 3.8e
0; Mismatches
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
TYPE: amino acid*
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
CORRESPONDENCE ADDRESS: ADDRESSE: & ADDRESSEE: & Clauber &
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JS-07-755-161A-3
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APPLICANT: YAMANOTO, NAOKI
APPLICANT: NAKASHMA, HIDEKI
APPLICANT: NAKASHMA, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANABAKI, YOSHHHRO
APPLICANT: NANABAKI, YOSHHHRO
APPLICANT: NANABRA OF SEQUENCES:
ANDRESSEE: PATENT ADMINISTRATOR, TESTA, HURMITZ &
ADDRESSEE: THIERAUUT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.0%; Score 64; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               DATE:
DOCUMENT NUMBER:
PILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/08204487; Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CFOWORNMRKVR 13
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                    ISSUE:
PAGES:
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                          Indels
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US-07-891-174-3
US-07-891-174-3
Sequence 3, Application US/07891174
SUMMERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
CITY: Weshington STATE: D.C.
CONFUTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-NAY-1992
CLASSIFICATION NAT:
FILING DATE: 29-NAY-1992
CLASSIFICATION DATA:
APPLICATION DATE:
APPLICATION DATE:
ATORNER: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33-367
REFERENCE/DOCKET NUMBER:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
TELECHOMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INPORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acide TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL ITYPE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                   1 CFQWQRXMRKVR 12
                                                                                                               2 CFOWORNWRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                      ò
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LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
MUTHORS:
MUTHORS:
MUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRIE READMELE FORM:
COMPUTER READMELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE: O2-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: CAMPBELL, PAULA A.
REFERENCE/DOCKET NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
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LOCATION:

1 IDENTIFICATION METHOD:

1 OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"

US-08-256-771-25
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                                     Length 20;
                                     97.0%; Score 64; DB 1;
91.7%; Pred. No. 4.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PELLING DATE: JULY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAZTEN INFORMATION:
REGESTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                   Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                               1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRXMRKVR 12
                                                                                                                                                  2 CFOWORNWRKVR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: Bir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                        RESULT 9
US-08-256-771-25
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US-08-381-984-24
   US-08-256-771-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 24, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: PRODUCTS THEREMITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE SECURENCE, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D. C.
COUWTRY: U.S.A.
ZIP: 20005.A.
                                                                                                                                                                                                                                                                                  97:0%; Score 64; DB 1; Length 20; 91.7%; Pred. No. 4.2e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                        /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPERTAINS SILEM! "A-LOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/25/ELLING DATE: July 22, 1994 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: RAFEFERNCE/DOCKET NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relecommunication information:
    Telephone: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear WOLECULE TYPE: peptide
                                                                                                                                              FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /
OTHER INFORMATION: D
                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-08-256-771-24
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Gaps

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RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Sequence 4, Application US/09508734
; Patent No. 6423509
; Patent No. 6423509
; GENERAL INFORMATION:
    APPLICANT: Samyang Genex Corporation
    TILE OF INVENTION: Useful microorganism thereof
    TILE OF INVENTION: Useful microorganism thereof
    TILLE OF INVENTION: Useful microorganism thereof
    TILLE OF INVENTION: US-000-06-01
    TILLE OF INVENTION: DATE: 2000-06-01
    FURRENT APPLICATION NUMBER: PCT/RR99/00373
    PRIOR FILING DATE: 1999-07-14
    PRIOR FILING DATE: 1998-07-14
    PRIOR FILING DATE: 1998-07-13
    SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as a fragment therew
OTHER INFORMATION: peptides including the specified peptide as a fragment therew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.0%; Score 64; DB 1; 1
illarity 91.7%; Pred. No. 4.2e-05;
Conservative 0; Mismatches 1:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION 252
PRIOR APPLICATION DATA:
APPLICATION DATA:
                       805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CFÓWÓRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                  Washington
                                                                                    STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
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NAME/KET:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
CTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
DEBNIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions of the information and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.0%; Score 64; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.2e-05; Matches 11; Conservative 0; Mismatches 1; Indels
Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Ammoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTY: U.S.A.
ZIP: 20005
ZIP: 20005
ZIP: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
NUMBER OF SEQUENCES: ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWORXMRKVR 12
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US-08-381-984-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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NAME/KEY: modified site

LOCATION: 21

LOCATION: 21

LOCATION: 21

OTHER INFORMATION: Cyg residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cyg residue at location 4"
AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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91.7%; Pred. No. 5.2e-05;
.ive 0; Mismatches 1;
   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAZTEN N. CHECK Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                                                                                                                                                                                                                             10:
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LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cyg rei
OTHER INFORMATION: thiol:
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                STRANDENNESS SHIP
STRANDENNESS SHIP
TOPOLOGY: linear
MYLOTHETICAL:
ANTI-SENSE:
FRAGNENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORXMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
1S-09-508-734-6
1S-09-508-734-6
1Patent No. 6423509
1GENERAL INFORMATION:
1GENERAL INFORMATION:
1TITLE OF INVENTION:
1TITLE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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0
                                                                                                                                           Query Match 97.0%; Score 64; DB 4; Length 22; Best Local Similarity 91.7%; Pred. No. 4.6e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 64; DB 4; Length 24;
Pred. No. 5e-05;
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IS-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
ONTRESPONDENCE ADDRESS:
ADDRESSEE: Wendercth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: MSA Compatible
COMPUTER: NEADBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: NEADBLE FORM:
MEDIUM SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
                           TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                       1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
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LENGTH: 22
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Gaps

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OTHER INFORMATION: ()note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                     97.0%; Score 64; DB 1; Length 25; 91.7%; Pred. No. 5.2e-05; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 21, 2003, 08:04:26 Job time : 8.93023 secs
                                                                                                                                                                                                                                                                               FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                    DATE:
DOCUMENT NUMBER:
                                                                                                                       TITLE:
JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "thiol group of Cys residue at location 4 connected by disulfide bond with thiol group of Cys residue at location 21"
              Sequence 10, Application US/07891174
Sequence 10, Application US/07891174
Sequence 10. Application US/07891174
Sequence 10. Sat7084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: BO. A. A.
ZIP: 20005
COUNTRY: U.S.A.
ZIP: 20005
CONDUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
CONTURER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
CONTURER I EM Compatible
OPERATION STORES: US/07/891,174
APPLICATION NUMBER: US/07/891,174
FILING DATE: D-MAX-1992
CLASSIFICATION NUMBER: US O7/755,161
ATTORARY AGENT INFORMATION:
APPLICATION NUMBER: US O7/755,161
ATTORARY AGENT INFORMATION:
APPLICATION NUMBER: US OFFER FERRENCE/DOCKET NUMBER:
ATTORARY AGENT INFORMATION:
NAME: Waarren M. Cheek US.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELEPHONE: 202-371-8856
TELEPHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
NAME/KEY:
A LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: / note-
OTHER INFORMATION: / forter
OTHER INFORMATION: thiol (FEATURE):
NAME/KEY: modified site
LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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HYPOTHETICAL:
RANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                JS-07-891-174-10
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Sequence 16, Appl Sequence 17, Appl Sequence 10, Appli Sequence 6, Appli Sequence 7, Appli Sequence 1, Appli Sequence 11, Appli Sequence 2, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli

Sequence 24, Sequence 21, Sequence 4,

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Score 64; DB 9; Length 15;
Pred. No. 2.5e-05;
0; Mismatches 1; Indels
10 US-09-904-536-14

10 US-09-904-536-15

10 US-09-904-536-16

10 US-09-904-536-18

10 US-09-904-536-10

10 US-09-904-65-5

10 US-09-908-65-5

10 US-09-864-761-4837

10 US-09-864-761-4837

10 US-09-908-869-26

10 US-09-908-869-26

10 US-09-908-869-28

10 US-09-908-869-28

10 US-09-798-869-10

10 US-09-798-869-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SQUENCE 2, Application US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION:
| APPLICANT: JOHN SIGGED SVENDSEN
| APPLICANT: GYSTEIN REKDAL
| APPLICANT: EALDUR SVEINAD (RNSON)
| APPLICANT: LARS VORLAND
| TITLE OF INVENTION: BIOACTUR PEPTIDES
| TITLE OF INVENTION: BIOACTUR PEPTIDES
| CURRENT APPLICATION NUMBER: US/09/798,869
| CURRENT PILING DATE: 1999-08-31
| PRIOR FILING DATE: 1998-08-31
| SOFTWARE: PASTSEQ for Windows Version 4.0
| SEQIED NOS: 30
| TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REKOAL); APPLICANT: BALDUR SVEINBJ(RNSSON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.08;
     Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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; ORGANISM: HOMO SAPIENS
US-09-798-869-2
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    RESULT 2
US-09-798-869-20
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Sequence 3, Appli
Sequence 23, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 21, Appli
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                                                                                          February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8,
Sequence 9,
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1: \cgn2_6/prodata/2/pubpaa/USOB NEW PUB.pep:*

2: \cgn2_6/prodata/2/pubpaa/PUB.WW PUB.pep:*

3: \cgn2_6/prodata/2/pubpaa/PUB.WW PUB.pep:*

4: \cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*

5: \cgn2_6/prodata/2/pubpaa/USO6_NEW PUB.pep:*

6: \cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

7: \cgn2_6/prodata/2/pubpaa/USO7_PUBCOMB.pep:*

8: \cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

9: \cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

10: \cgn2_6/prodata/2/pubpaa/USO9_NEW PUB.pep:*

11: \cgn2_6/prodata/2/pubpaa/USO9_NEW PUB.pep:*

11: \cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: \cgn2_6/prodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: \cgn2_6/prodata/2/pubpaa/USO9_NEW PUB.pep:*

14: \cgn2_6/prodata/2/pubpaa/USSO NEW PUB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-798-869-2
US-10-02-398-869-6
US-09-798-869-3
US-09-798-869-3
US-09-798-869-3
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-8
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US-09-798-869-8
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US-09-798-869-30
US-09-798-869-30
US-09-798-869-30
US-09-888-320-2
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US-09-904-536-9
US-09-904-536-11
US-09-904-536-12
US-09-904-536-13
                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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66
1 CFQWQRXMRKVR 12
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
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Maximum DB seq
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Gaps

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TYPE: PRT ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity 91.,
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Best Local Similarity 83.3
Matches 10; Conservative
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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kurzel, Tomasz
APPLICANT: Kurzel, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Obyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Jacobson, Price, Holman & Stern
STERT: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                             97.0%; Score 64; DB 9; Length 25; 91.7%; Pred. No. 4.1e-05;
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MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORY disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: TBM PC DOS, MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US/08/724,586
FILING DATE: 05-MAY-1994
ATTORNEY, AGENT INFORMATION:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 05-MAY-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
             APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE BERERNES: A14049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REBERENCE/DOCKET NUMBER: 10501
TELECOMMUNICATION INFORMATION:
TELEPHOR: (202) 393-5360
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 400 Seventh St
CITY: Washington D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRXMRKVR 12
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0
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0
Length 694;
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97.0%; Score 64; DB 9; 1
91.7%; Pred. No. 0.00096;
iive 0; Mismatches 1;
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Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                           Publication US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OGIN SIGURD SUENDERN
APPLICANT: GYSTEIN REXCAL
APPLICANT: BALDUR SVEINBAI (RNSSON
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BICACTIVE PEPTIDES
ITILE REPERBNCE: A34049-PCT-USA-A
CURRENT PILING DATE: 2001-02-27
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PG7/GB99/02861
PRIOR PILING DATE: 1999-08-11
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABELSEQ for Windows Version 4.0
SSOFTWARE: FABELSEQ for Windows Version 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09798869

Publication No. USZ0030022821A1

GENERAL INFORMATICN: OBCUSE SELAI

APPLICANT: OFN SIGNED SVENDSEN

APPLICANT: ASLDUR SVEINBAJ (RNSSON

APPLICANT: BALDUR SVEINBAJ (RNSSON

APPLICANT: BALDUR SVEINBAD TITLE OF INFORMATION BLOACH STORE

TITLE OF INFORMATION: BIOACTIVE PEPTIDES

TITLE PEFERNCE: A34449-POT-USA-A

CURRENT FILING DATE: 2001-02-27

PRIOR PELING DATE: 1999-08-31

PRIOR APPLICATION NUMBER: PCT/GB99/02851

PRIOR APPLICATION NUMBER: BRICK APPLICATION NUMBER: GB9918938.4

PRIOR APPLICATION NUMBER: GB9918938.4

PRIOR APPLICATION NUMBER: GB9918938.4

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SSOFTWARE: FastSEQ for Windows Version 4.0

SSO ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80.3%;
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Best Local Similarity
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Gaps
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Pred. No. 0.12;
1, Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 9;
Pred. No. 0.077;
1; Mismatches
                                                                                                                                                                                                     APPLICANT: JUNE SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPPLIDES
FILE REPERENCE: 345049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CTJGB99/02851
PRIOR APPLICATION NUMBER: GB9818938-4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFREENCE: A34049-PCT-USA-A
CURRENT PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GE99/02851
PRIOR APPLICATION NUMBER: PCT/GE99/02851
PRIOR APPLICATION NUMBER: GE9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                  Sequence 4, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CLRWQNEMRKV 13
1 CFQWQRXMRKV 11
                                         3 CYÓWOWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQWQRXMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORXMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: MURINE
US-09-798-869-22
                                                                                                      RESULT 8
US-09-798-869-4
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: synthetic peptide (modified form of homo sapiens OTHER INFORMATION: sequence)
1S-09-798-869-7
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Pred. No. 0.0034;
2; Mismatches 1; Indels
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1; Indels
                                                                                                                                      ESULT 6
19-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US2003002281A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSIN
APPLICANT: (YSTEIN RENDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A3404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: POT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INPORMATION:
APPLICANT: OF SIGURD SUENDER
APPLICANT: (YSTEIN REKOAL
APPLICANT: (YSTEIN REKOAL
APPLICANT: LARS VORLAND
TITLE OF INVENTON: BIOTON: BOOTON'S SUENDER
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FSECSEE FOR WINDOWS VERSION 4.0
SEQ ID NO 7
SEQ ID NO 7
LENGTH: 15
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.3%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CYQWQRRMRKL 13
                                       CFOWORXMRKV 11
                                                                              3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: CAPRINE
IS-09-798-869-23
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1S-09-798-869-7
Matches
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1 CFQWQRXMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine
OTHER INFORMATION: sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.1%; Score 41; DB 9; Length 15; llarity 63.6%; Pred. No. 0.26; Conservative 1; Mismatches 3; Indels
Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OTHN STGUED SVENDERN
APPLICANT: EALDUR SVEINBLEN
APPLICANT: BALDUR SVEINBLEN
TILLE OF INVENTION: BIOACTIVE PEPTIDES
TILE OF INVENTION: BIOACTIVE PEPTIDES
TILE OF INVENTION: BIOACTIVE PEPTIDES
TOURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
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Sequence 29, Application US/09798669
FUBLICATION OF US20030022821A1
APPLICATION OF USCONDING SIGNED
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: ALAES VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPRENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRXMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29
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US-09-798-869-30
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LENGTH: 15
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LENGTH: 15
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SUBJECTANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hansel, David K.
APPLICANT: Hansel, David K.
APPLICANT: Ghen, Wensheng
TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: UNGBER: US 60/180,312
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-01-30
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Pred. No. 0.26;
3; Mismatches 2; Indels
                                                        APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN REKEAL
APPLICANT: AALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: AALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTURE PEPTIDES
FILE REFERENCE: A34049-CT-UGA-A9, CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: B989-08-31
PRIOR APPLICATION NUMBER: B989-08-31
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastERQ for Windows Version 4.0
SOFTWARE: FastERQ for Windows Version 4.0
SCROID NO 30
LENGTH: 15
TYPE: PRT
TYPE: PRT
CRAMISM: BOVINE
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR PILING DATE: 2001-01-30
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US20030022821A:
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Best Local Similarity 54.5
Best Local Similarity 6.
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APPLICANT: Bekker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
IS-09-888-120-2
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO AL096701.14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EST_HUMAN HIT: AM294800.1, EVALUE 1.00e-06
IS-09-864-761-47985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3%; Pred. No. 1.8;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.1%; Score 37; DB 9; Length 489; 54.5%; Pred. No. 35; ive 2; Mismatches 3; Indels
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN VEY. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09888320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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JS-09-888-320-2
                                                                                                                                                                                                                                                                              TYPE: PRT
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Matches
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ESULT 15 'S-09-904-536-8 Sequence 8, Application US/09904536 Patent No. US20020111475A1

GENERAL INFORMATION

253 COKWPRRMRKM 263

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APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T.

ITLLE OF INVENTION: FLI3-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/904,536
CURRENT FILING DATE: 2001-07-16
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 201
SOFTWARE: Patentin Ver. 2.1
SOFTWARE:
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lactotransferrin p
lactoferrin goat
lactoferrin goat
lactoferrin precur
dynein beta heavy
hypothetical prote
hypothetical prote
hypothetical prote
pyridoxamine 5'-ph
pridoxamine 5'-ph
pridoxamine 5'-ph
pridoxamine 5'-ph
probable pyridoxam
3.3K hypothetical
grochrome P450 ho
cytochrome P450 ho
polymyxin B resist
hypothetical prote
signal peptidase I
hypothetical prote
signal peptidase I
hypothetical prote
fila ligand - huma
interleukin-2 rece
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hypothetical prote
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protein F09C3.1 [i
F1511.22 [imported
pyridoxamine-phosp
                                                                                                                                                              February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries
                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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1: pir1:*
2: pir2:*
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fprA protein - Myx	hypothetical prote	cell cycle arrest	ornithine decarbox	probable cytochrom	cytochrome P450-li	cytochrome P450 ho	cytochrome P450-li	cytochrome P450 mo	hypothetical prote	hypothetical prote	finger protein unk	hypothetical prote	kinase-related pro	protein F21H11.2 [	carcinoembryonic a
T10126	AD2346	A39654	S52784	B96691	B85441	T04730	C85441	T52174	AB0858	T24218	S42526	D83181	A35774	D88450	D33876
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53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	51.5
				35							32				
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

TFHUL  Igatotransferrin precursor [validated] - human  Igatotransferrin precursor [validated] - human  C.Becies: Homo sapiens (man)  C.Becies: Homo sapiens (man)  C.Becies: Homo sapiens (man)  C.Accession: Glu344, SI1228, A4401; SI0324; SI5853; S20841; S07160; AR  R.Cho. V.: Glu344, SI1228, A4401; SI0324, SI5853; S20841; S07160; AR  R.Cho. V.: Glu394, SI1228, A4401; SI0324, SI5853; S20841; S07160; AR  A.Recience number: G06820  A.Accession: Glu394  A.Molecule type: mRMA  A.Molecule: 1-711 - CRUO  A.TCEGATE CONDITION  A.Recience number: SI1228, MID:9457286; PIDN:AAB60324.1; PID:946'  B.Rey, M. M.; Wolcohuk, S. L.; Gaboer, H.A.; Pieper, F.R.  N.Claic Axid Sess 10, S208, 1990  A.TIELS: Condition: SI1228, MID:9084839; PMID:2402455  A.Recension: SI1228, MID:9084839; PMID:2402455  A.Recension: SI1228, MID:9084839; PMID:240245;  A.Recension: SI1228, MID:9084839; PMID:2402455  A.Recension: SI1228, MID:9084839; PMID:2402455  A.Recension: SI1228, MID:9084839; PMID:2402455  A.Recension: SI1228, MID:9084839; PMID:240245;  A.Recension: SI1228, MID:9084839; PMID:2402485  A.Recension: SI1228, MID:9084839; PMID:2402487; PID:926333  A.Recension: SI1228, MID:93125571; PMID:1480183  A.Recension: SI1228, MID:9312551; PMID:13026333  A.Recension: SI1228, MID:9312551; PMID:2374734  A.Recension: SI1224, MID:9312559; PMID:2374734  A.Recension: SI1224, MID:9312559; PMID:2374734  A.Recension: SI1034  A.Recension: SI1034	RESULT 1  Inactornasferrin precursor [validated] - human  Inactornasferrin precursor [validated] - human  C. M. Hermate names   Lactoferrin  C. Species   M. A. Hermate names   Lactoferrin  C. Date: 31-Mar-192   Ractoferrin  R. Cho. Subject not be RBIL Data Library, March 1994  A. Recession: G01394   S11228; A45401; S10324; S15833; S20841; S07160; A61169; A31000; S74  R. Cho. Subject not be RBIL Data Library, March 1994  A. Recession: G01394  A. Recession: G01394  A. Recession: G01394  A. Recession: S11228   WID: G467236; PIDN: AAB60324.1; PID: G467237  R. Rey, M. W. W. Poloshuk, S. L.; Geboer, H.A.; Pieper, F.R.  Nucleic Acids Res. 18, 5289, 1990  A. Recession: S11228   WID: 90384839, PMID: 2402455  A. Recession: S11228   WID: 90384839, PMID: 2402455  A. Recession: S11228   WID: 90384839, PMID: 2402455  A. Recession: S11289  A. Recession: A45401  A. Recession: A45401
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Length 708;

DB 2;

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80.3%; Score 53; DB llarity 72.7%; Pred. No. 0.08 Conservative 2; Mismatches
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R;Liu, Y.; Teng, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                        1 CFQWQRXMRKV 11
                                                                                                                                                                                                                                                                                                             38 CYQWQRRMRKL 48
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Matches 7; Conserv
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Best Local Similarity
Matches 8, Conserv
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A;Residues: 3-707 <PEN>
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C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; transferrin; iron binding; milk
C; Reywords: duplication; glycoprotein; iron binding; milk
C; Reywords: duplication; glycoprotein; iron binding; milk
C; Reywords: duplication; glycoprotein; grequence #status experimental <MAT>
C; Reywords: lactotransferrin repeat homology <TRH1>
C; Rey Sonain: transferrin repeat homology <TRH1>
C; Rey Sonain: transferrin repeat homology <TRH2>
C; R
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Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
Afritle: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A; Accession: JC2323; MUID:94380047; PMID:8093048
A; Accession: JC2323
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 436-487, A', 489-711 <RAD>
A; Residues: 456-487, A', 489-711 <RAD>
A; Cross-references: EMBL: MN8642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.G.; Liu, Y.; Hunng, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                  Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Residues: 3.70."."
", Experimental source: normal breast tissue
", Experimental source: normal breast tissue
", Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
"Ar. J. Blochem. 145, 659-666, 1984
", Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth ", Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .; Molecule type: protein ..., Molecule type: protein ..., 203, 'L', 205, 'K', 207-208,' K', 210-385,' Q', 387-391,' W', 393-4, Nesdudes: 20140,142-1169,171-203,' L', 205,' K', 207-208,' K', 210-385,' Q', 387-391,' W', 393-4, 1, Note: this is the final paper in a series ... Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L. Nacholt, 241, 393-308, 1996 ... 1996 ... Balochem: 241, 393-308, 1996 ... 1996 ... Thirle: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin ... Reference number: S74119; MUID:97054624; PMID:8898921
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Reference number: S07160.
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F:359-696/Domain: transferrin repeat homology <TRH2>
F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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Pred. No. 0.00083;
0; Mismatches 1; Indels
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A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
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Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
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Cross-references: GDB:119368; OMIM:150210
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S74119
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Jactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
A;Tile: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NyAlternate names: lactorizansferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A29438; A41205
R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactorizansferrin is the major estrogen inducible protein of mouse uterine secritization: A;Reference number: A92596; MuID:87280033; PMID:3611056
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J. Biol. Chem. 266, 21880-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
A;Accession: A41205
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A, Residues: 1-15 < LIU>
A, Cross-references: GB:M/47/8
C, Superfamily: transferrin; transferrin repeat homology
C, Keywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-707/Product: lactotransferrin #status predicted <MAT>F;358-695/Domain: transferrin repeat homology <TRH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Status: preliminary
A; Molecule type: protein
A; Residues: 1-33 < QIA.
C; Superfamily: transferrin; transferrin repeat homology
C; Keywords: duplication
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Pred. No. 0.016;
3; Mismatches
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beta heavy chain - Chlamydomonas reinhardtii

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A,Map position: 5
A,Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 59¢
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
R;Goodner, B: Hinkle, G: Gattung, S: Miller, N: Blanchard, M: Qurollo, B:; Goldman, A:; Liu, F:; Wollam, C:; Allinger, M: Doughty, D:; Scott, C:; Lappas, C:; Markelz, B., Science 294, 223-2238, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell starp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, 
C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
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A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAX86569.1; PID:g15155733; GSPDB:GN00169
                                                                                                                                                                                                                       A)Status: preliminary; translated from GB/EMBL/DDBJ
A)AOlecule type: DNA
A)Residues: 1-932 - 878
A)Residues: ISBZ: 1932 - 878
A)Residues: EMBL: US0308; PIDN: AAC48001.1; GSPDB: GN00023; CESP: F07C3.1
A)Experimental source: strain Bristol N2; clone F07C3
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Pred. No. 25;
1; Mismatches 3; Indels
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R;Favello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
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A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                          A; Reference number: Z20528
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A;Molecule type: DNA
A;Residues: 1-206 <KUR>
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A; Interposition: IX
A; Interposition: IX
A; Interposition: IX
A; Interposition: IX
B; Interposition: IX
B; Interposition: Interposition:
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R,Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: Z16302; MUID:94274778; PMID:8006077
A;Accession: T08030
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Status: preliminary; translated from GB/EMBL/DDBJ
MOLecule type: DNA
Residues: 1-275 < WILL
CTOSE-references: EMBL: Z81089; PIDN: CAB03137.1; GSPDB: GN00028; CESP: F53H4.4
Experimental source: clone F53H4
                                                                                                                                                                              Species: Chlamydomonas reinhardtii
Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: translated from GB/EMBL/DDBJ
Molecule: type: DNA
Residuae: 1-4568 <MIT>
Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
Experimental source: strain 21gr
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Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
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J.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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4,Introns: 67/1; 153/1
2,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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Ribobson, R. submitted to the EMBL Data Library, October 1996 A,Reference number: 219587

Gene: CESP: F53H4.4

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hypothetical protein F07C3.1

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cytochrome P450 homolog At2g23190 - Arabidopsis thaliana (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Ol-Feb-1999 #sequence_revision Ol-Feb-1999 #text_change 23-Mar-2001 (Cispecies: Ol-Feb-1999) #text_change 23-Mar-2001 (Cispecies: Ol-Feb-1999) #text_change 23-Mar-2001 (Cispecies: Ol-Feb-1997) * Albarana Chounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau. Bubhitted to the EMBL Data Library, November 1997 Albescription: Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence. AlReference number: 214164
                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence revision 01-Feb-1999 #text_change 23-Mar-2001
C;Accession: T00510; A84622
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau submitted to the EMBL Data Library, November 1997
A;Description: Arabidopsis thallana chromosome II BAC T20D16 genomic sequence.
A;Reference number: Z14164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ibin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, Luss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, ature 402, 761-768, 1999
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A;Experimental source: cultivar Columbia
R;Lih, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
K.; X, Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GB:AE002093; NID:g2642441; PIDN:AAB87109.1; GSPDB:GN00139
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                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                  - Arabidopsis thaliana
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Length 289
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A,Status: translated from GB/EMBL/DDBJ
A,Residuss: 1-515 -ROD
A,Coss-reference: EMBL:AC002391; NID:g2642421; PID:g2642441
A,Experimental source: cultivar Columbia
DB 2;
19;
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Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  cytochrome P450 At2g23220 [imported]
Score 38;
Pred. No. 1
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A, Molecule type: DNA
A, Residues: 1-543 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
57.6%;
larity 50.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: At2g23220; T20D16.15
                                                                                                                                72
                                                                                                                                                                                             8 CFTWEEYARHVR 19
                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary
Molecule type: DNA
Residues: 1-515 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map position: 2
Introns: 182/3; 310/3
                                                                                                                                1 CPOWORXMRKVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 CFEWOR 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T00510
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   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J. Mazur, M.; Goltsman, B.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:1175668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RiTheologia, A.; Bcker, J.R.; Palm, C.J.; Rederspiel, N.A.; Kaul, S.; White, O.; Alonso, ansh. C.W.; Chung, M.K.; Palm, C.J.; Rederspiel, N.A.; Kaul, S.; White, O.; Alonso, ansh. N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Rature 408, 816-820, 2000
C.A.; Huter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.M.
A;Title. Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G86403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis (#
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Nolecule type: DNA
Residues: 1-200 «KUR»
Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:917983525; GSPDB:GN00190
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Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
A; Cross-references: GB: AE008688; PIDN: AAL41776.1; PID: 917739129; GSPDB: GN00186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Brucella melitensis
Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3K hypothetical protein F28L5.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                 59.1%; Score 39; DB 2;
Larity 50.0%; Pred, No. 9;
Conservative 2; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                             A,Gene: pdxH
A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
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Pred. No.
                                   Experimental source: strain C58 (Dupont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.1%;
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CFHWKSLRRQVR 99
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Best Local Similarity
Matches 6; Conserv
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A;Residues: 1-85 <PAR>
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h. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
tature 413, 848-852, 2001
**Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
**Jitle: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy
**Neference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: T14803
Thilds, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet, Millet to the EMBL Data Library, April 1996
Reference number: Z18186
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ture 402, 761-768, 1999
Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                              Status: preliminary
Molecule (type: DD)
Residues: 1-543 <STO>
Cross_references: GB:AE002093; NID:g2642444; PIDN:AAB87112.1; GSPDB:GN00139
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obce: this species has also been called Salmonella typhi
bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
ccession: AG0794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Sorghum bicolor (sorghum)
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          Whap position: 2

%Introns: 211/3; 339/3

%Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

%Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology

%;341-500/Domain: cytochrome P450 homology <P45>

%;478/Binding site: heme iron (Cys) (axial ligand) #status predicted
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57.6%; Score 38; DB 2; Length 1135;
Best Local Similarity 36.4%; Pred. No. 69;
Matches 4; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.6%; Score 38; DB 2; Length 543;
83.3%; Pred. No. 34;
tive 1; Mismatches 0; Indels
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Molecule type: mRNA
Residues: 1-1135 <CHI>
Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
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Best Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                    Gene: T20D16.18; At2g23190
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775 CLEWNKAMQKI 785
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A;Cross-references: GB:AL513382; PIDN:CAD07537.1; PID:g16503529; GSPDB:GN00176
C;Genetics:
A;Gene: pmrD
                                                                                   Length 85;
                                                                                Score 37; DB 2;
Pred. No. 8.9;
1; Mismatches
                                                                                                                                                                                                                                                                        Search completed: February 21, 2003, 08:02:45 Job time : 11.6047 secs
                                                                                Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                   1 CFQWQRXMRK 10
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Quite7 schiosacch P5046 escherichia P1462 sus scrofa Q41046 pinus sylve Q2432 drosophila Q24595 drosophila P13368 drosophila P24674 ascaris suu P2167 escherichia Q06399 salmonella

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Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Mammary gland;
MEDLINE-90384839; PubMed=2402455;
MEDLINE-90384839; PubMed=2402455;
MCDLINE-90384839; PubMed=2402405;
MCOMPLE- nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                         11-JUL-1996 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin Lactoferroxin B; Lactoferroxin C)
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Mammary gland;
Liang Q., Jimenez-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBark/DDBJ databases.
                                                                                                                                                                                                                                                               TRFL HUMAN STANDARD, PRT; 711 AA.
P02788; Q16780; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUB=Mammary gland;
TISSUB=Mammary gland;
TISSUB d., Chen X., Huan L.;
"Chang H., Chen X. Huan L.;
"Chong H., Chen X. Huan L.;
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conneely O.M.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences.";
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                              ALIGNMENTS
             YEBA HAEIN
MSS1_SCHPO
AER_ECOLI
                                                     TRFL PIG
PHY PINSY
T2D2 DROME
                                                                                                         7LES DROME
NULM ASCSU
YEDD ECOLI
                                                                                                                                                   YEDD SALTY
                                                                                                DROME
 428
4458
4475
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12133
1293
777
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TISSUE=Mammary gland;
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SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
 Cho Y.Y.;
 escherichia
homo sapien
variola vir
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drosophila
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Q9tum0 camelus dro
Q29477 capra hircu
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homo sapien
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                                                                                          February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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P01589 |
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P16710
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McCombie W.R., Wilson R., Chen B., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen B., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/Genbank/DDBJ databases.
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MEDLINE=90064528; PubMed=258556;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
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of
                                                                                                                                                                                                                Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J., Jolles P.,
                                                                                                                                                                                                                                                                                                                        MEDLINE-82262043; PubMed-7049727;
Mecz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                            "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains."; Biochim. Biophys. Acta 670:243-254(1981),
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MEDLINE=88001031, PubMed=3477300;
Rado I.A., Wel X., Benz E.J. Jr.
"Isolation of lactoferrin CDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
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MEDLINE-82046817; PubMed=6794640;
                                                                                    SEQUENCE OF 20-711.
MEDLINE-85076667; PubMed=6510420;
MEDLINE-85076667; PubMed=6510420;
MEDLINE-85076667; Orlles J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                               'An 88 amino acid long C-terminal sequence of human
                                                "Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013 (1990).
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MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                      comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
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           TISSUE=Mammary gland,
mbDLINE=20326549; PubMed=2374734;
POWell M.J., Ogden J.E.;
"Nucleotide sequence of human lac!
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SEQUENCE OF 3-711 FROM N.A.
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TISSTE-Mammary gland;
Lee T. S. Kim S. Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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IRON 2 (BY SIMILARITY)
ANION (BY SI
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TISSUE-Mammary gland;
MEDLINE-94380047; PubMed=8093048;
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708 AA;
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Sukaryota, Metazoa, Chordate, Craniata, Vertebrate, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Somali; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
int. Dairy J. 9:481-466(1999)
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PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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                 Score 64; DB 1; Length 711;
Pred. No. 0.00024;
0; Mismatches 1; Indels
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16-0CT-2001 (Rel. 40, Last sequence update)
15-0W1-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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RBL, AF165879, AAF82241.1, -.
HSSP, O77811, 1B1X.
InterPro, IPR001156, Transferrin.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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"Characterization of the goat lactoferrin cDNA. Assignment of the relaxacterization of the goat lactoferrin cDNA. Assignment of the relaxacterization of the goat lactoferrin cDNA. Assignment of the relaxacterization of the goat lactoferrin cDNA. Assignment of the blochem. Biophys. Res. Commun. 203:1324-1332(1994).

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                          Capra hircus (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae, Caprinae; Capra.
RESULT 3
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ID TREL
DAC 229477
DT 15-DEC
DT 15-D
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Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                               TRFL MOUSE STANDARD; PRT; 707 AA. P008071; P70890; Q912P2; Q1-ANG-1988 (Rel. 08, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMED custation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL, X78902; CAA55517.1; --
HSSP, O77699; ICE2.
InterPro; IPRO1156; Transferrin.
Pfam; PR00405; transferrin; 2.
Pfam; PR00405; TRANSFERRIN.
SMART; SW00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.
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C -> K (IN REF. 2).

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N-LINKED (GLCNAC. . . )
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN
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Liu Y., Teng C.T.;
"Characterization of estrogen_responsive mouse lactoferrin promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 266:21880-21885 (1951).
-!- FUNCTION: TRANSFEREINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USTALLY BICARBONATE.
-!- SUBINIT: MONOMER.
-!- SUBCELLUAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
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PIR; A28438; A28438.

R HSSP; P027881; LDE.

R MGD; MGI:96837; Ltf.

R InterPro; IPR001256; Transferrin.

P Fam; PR00405; transferrin.

R PR091TS; PR00425; TRANSFERRIN.

R SMART; SM00094; TR FER; P.

R PROSITE; PS00206; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN.2; 2.

R PROSITE; PS00207; TRANSFERRIN.2; 2.

R PROSITE; PS00207; TRANSFERRIN.3; 2.

Y Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
                                                             Pentecost B.T., Teng C.T., ^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                    Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN.
1.
                                                                                                                                                           Biol. Chem. 262:10134-10139(1987).
TISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, J03298; AAA40525.1; -.
EMBL, D88510; BAA13633.1; -.
EMBL, BC006904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-14 FROM N.A.
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"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
resolution.", Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.,
resolution.", 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBCELLAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Mammalia, Butheria, Perissodactyla, Equidae, Equus.
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COILED COIL (POTENTIAL).
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InterPro; IPR004273; Dynein_heavy.
Edm, PF03028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43; DB 1; Length 4568; Pred. No. 11; 3; Mismatches 3; Indels
     -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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ATP (POTENTIAL).
ATP (POTENTIAL).
MW; 9A9A5393C7C36AE7 CRC64;
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 38, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
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J. Cell SGA: 107:615-644(1994).

1. Cell SGA: 107:615-644(1994).

1. PUNCTION: FORCE GENERATING PROTEIN OF BUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS ATTAKAE ACTIVITY.

1. SUBDNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitchell D.R., Brown K.S.,
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
0DA4 OR ODA-4 OR SUP1.
Eukaryota, Varidiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceee; Chlamydomonad.
Chlamydomonadaceee; Chlamydomonas.
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ANION (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M-LINKED (GLCNAC. .) (POTENTIAL).
MR -> IQG (IN REF. 1).
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F26AE0340A4C19A8 CRC64;
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M-LINKED (GLCNA,
MR -> 100 (IN RE, 2)
M -> L (IN REF, 2)
R -> T (IN REF, 2)
R -> G (IN REF, 2)
R -> G (IN REF, 2)
R -> G (IN REF, 1)
R -> G (IN REF, 1)
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63.6%; Pred. No. 1.1;
ive 1; Mismatches
2.
BY SIMILARITY.
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MEDLINE=94274778; PubMed=8006077;
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Best Local Similarity 63.0
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4413
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707 AA;
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R PDB; 1B1X; 02-DEC.98.

R PDB; 1B1X; 02-DEC.98.

R PDB; 1B7Z; 02-FEB-99.

R InterPro; 1PR001156; Transferrin.

R Pfan; PF00405; Transferrin; 2.

R PRINTS; PR00423; TRANSFERRIN.

R PROSITE; PS00206; TRANSFERRIN 1; 2.

R PROSITE; PS00206; TRANSFERRIN 2; 2.

R PROSITE; PS00206; TRANSFERRIN 3; 1.

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07BB94D50E1B165D CRC64;
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Pred. No. 9.3;
3; Mismatches
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58.3%;
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292 AA.

PRT;

NIA DROME STANDARD; Q9XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created)

NLA DROME ID NLA D AC Q9XZL DT 30-MA

RESULT 7

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STANDEMES TOWN NAME STANDERS OF THE R.A., BVADER C.A., GOCCAYNE J.D., AGENDERS C.E., Holf R.A., BVADER R.A., Galle R.F., Addams M.D., Celnikers S.E., Holf R.A., Brown R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburnar M., Henderson S.N., Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chelen L.X., Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chelen L.X., Sutton G.G., Wortman J.E., Tandell M.D., Zhang Q., Chelen L.X., Sutton G.G., Wortman J.E., Tandell M.D., Zhang Q., Chelen L.X., Brandon R.C., Ragers Y.-H.C., Blazej R.G., Chamanch C., Raldwin D., Ballew R.M., Basu A., Barnandel G., Bayraktaroglu L., Beasley E.M., Ballew R.M., Cawley B.C., Burdwin D., Ballew R.M., Cawley B.C., Burdwin D., Ballew R.M., Cawley B.C., Burdwin D., Bartin J.F., Dough E., Downes M., Deng E., Center A., Chandra I., Bartin J.E., Downes M., Deng E., Center A., Chang B., Delcher A., Cawley S., Dunkov B.C., Dunn P., Dodson K. V., Cawley S., Downes M., Dugan-Rocha S., Platschmann W., Rolson K.J., Evengeliste C.C., Ferriez C., Ferriera S., Fleischmann W., Dodson K.J., Bownes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dutchin K.J., Bvangeliste C.C., Ferriez C., Gabriellan A.E., Gorg F., Gorrell J.M., Well W., Well W., H., Ibegama C., Ander J. M., Harris M., Harris M.L., Harris M., Gong F., Gorrell J.M., Well W., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its modified on-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Haxapoda;

Insecta; Peerygota; Neopeera; Endopeerygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                     Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AF147700; AAD33987.1; -.
EMBL; AE003712; AAF55285.1; -.
FlyBase; FBGN0205629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
(Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                   females.
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PAS 1.
PAS 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LT2;
MEDLINE=94266712; PubMed=8206837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.6%;
36.4%;
SMART; SM00387; HATPase c;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 36.**,
Best Local 4; Conservative
                                                                                                                                                                                                                                                                             Repeat, Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     775 CLEWNKAMOKI 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRXMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella
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BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    DOMAIN
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PMRD SALTY
ID PMRD S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phytochrome B.";
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)
Plant Physiol. 113:611-619(1997)

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PRF FORM THAT
ABSORBS MAXIMALLY IN THE FAA-RED REGION. PHOTOCONVERSION OF PR IN
PFR INDUCES AMAXIMALLY IN THE FAA-RED REGION. PHOTOCONVERSION OF PR IN
PRESONVERSION OF PRE TO PR CANCELS THE INDUCTION OF THOSE
RESPONSES. PRR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE
BESPROSCHLOROPHYLLIDE REDUCTAGE, CHLOROPHYLL A/B BINDING PROTEIN,
PROTOCHLOROPHYLLIDE REDUCTAGE, THE SMALL SUBUNIT OF RIBULOSE
EXPRESSION OF ITS OWN GENES(S) IN A NEGATIVE PEEDBACK PASHION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukāryota, Viridiplantae, Streptophytā, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Panicoideae, Andropogoneae, Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-i- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILIA.
-i- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-i- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-i- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.B.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                     ö
             Score 38; DB 1; Length 292;
Pred. No. 6;
                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                      PRT; 1135 AA
        Query Match
Best Local Similarity 54.5%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (Sorghum) (Sorghum vulgare)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBLÍO 108/011 ABBELDENTI,
INTERPRO, IPRO03594 ATPLING_ATPRES.
INTERPRO; IPRO03018; GAF.
INTERPRO; IPRO04359; HIS KIN_
INTERPRO; IPRO04561; HIS KIN_
INTERPRO; IPRO01610; PAC_
INTERPRO; IPRO01010; PAC_
INTERPRO; IPRO01010; PAC_
PERM; PPO0160; phytochrome; I.
PERM; PPO0160; phytochrome; I.
PERM; PPO01899; PAS; Z.
PERM; PPO01899; PAS; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U56731; AAB41399.1; -
                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                150 FQWLRSFRRLR 160
                                                                                                                 2 FOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytochrome C.
                                                                                                                                                                                                                                                                                                PHYC SORBI
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Pfam; PF02518; HATPase c; 1. PRINTS; PR01033; PHYTOCHROME. SMART; SM00065; GAF; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001)
-!- FUNCTION: CONFERS RESISTANCE TO POLYMXXIN B. POLYMXXIN RESISTANCE
MAY BE MEDIATED BY AN INTERACTION BETWEEN PWRA OR A PWRA-REGULATED
GENE PRODUCT AND PWRD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=LTZ / SGSC1412 / ATCC 700720;
MEDLINE=Z1534948; Pubméd=11677609;
MEDLINE=Z1534948; Pubméd=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
SWART; SM00388; HisRA; I.
SWART; SM00086; PAC; 1.
SWART; SM00091; PAS; 2.
TIGREAMS; TIGRO0229; sensory box; 2.
PROSITE; PS50109; HIS KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50046; PHYTOCHROME 1; FALSE_NEG.
PROSITE; PS50046; PHYTOCHROME 2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roland K.L., Bether C.R., Spitznagel J.K.;
"Isolation and characterization of a gene, pmrD, from Salmonella typhimurium that confers resistance to polymyxin when expressed in multiple copies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typnimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 1135;
Pred. No. 23;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                     902 1122 HISTIDINE KINASE.
321 321 CHROMOPHORE (BY SIMILARITY).
1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-UWN-2002 (Rel. 41, Last annotation update)
POLYWXXIN B resistance protein pmrD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85 AA.
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235 AA.

PRT;

STANDARD;

HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=Nelspruit,
STRAIN=Nelspruit,
STRAIN=Nelspruit,
Planet P., Jagoueix S., Bove J.M., Garnier M.;
Detection and characterization of the African Citrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKaJL-
rposC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTIO
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRAITS.
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last ennotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liberibacter africanus (Liberobacter africanum).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Rhizobiaceae, Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA' CHAIN.
SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                          Score 37; DB 1; Length 85; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001572; RNA_pol_B.
Pfam; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                      StyGene; SG10304; pmrD.
Antibiotic resistance; Complete proteome.
SEQUENCE 85 AA; 9749 MW; 1E1922419EA5OCCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.1%; Score 37; DB 1; 60.0%; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 AA.
                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
EMBL; AE008803; AAL21205.1; -.
                                                                                                                                                              56.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U09675; AAA19557.1; -
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Best Local Similarity 60.v.
6, Conservative
                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                  1 CFQWQRXMRK 10
                                                                                                                                                                                                                                                                                                                                                                    74 CDEWORLTRK 83
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P41187;
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                                                                                                                                                                     Query Match
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secreted (isoform 2).
-i- ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bundles and cystine knots.";
Nat. Struct. Biol. 7:486-491(2000).
-!- FUNCTION: STIMULATES THE PROLIPERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.
-!- SUBUNIT: Homodimer (isoform 2).
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Pfam; PP02947; flt3_lig; 1.
Cytokine; Glycoprotein; Transmembrane; Alternative splicing; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDINE-94235842; PubMed-8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Brobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; "Cloning of the human homologue of the murine flt3 ligand: a growth factor for early hematopoietic progenitor cells."; Blood 83:2795-2801(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINES 49195428 PubMed=8145881;

Hannum C., Culpepper U., Campbell D., McClanahan T., Zurawski S.,

Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,

Bazan J.F., Kastelein R., Hudak S., Magner J., Mattson J., Luh J.,

Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,

Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,

Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.,

Ligand for Furj-YFLZ receptor tyrosine kinase regulates growth of

haematopoietic stem cells and is encoded by variant RNAs.";
                                                                                                                                                                                                                                                                                       Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20343011; PubMed=10881197;
Savvides S.N., Boone T., Karplus P.A.;
"Flt3 ligand structure and unexpected commonalities of helical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                          01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U04806; AAA17999.1; -. EMBL; U03858; AAA19825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U29874; AAA90949.1; -.
EMBL; U29874; AAA90950.1; -.
PDB; LETE; 09-JUN-00.
Genew; HGNC:3766; FLT3LG.
                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                igand) (Flt3L).
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure
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1 CFQWQRXMRK 10

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10 CVOWSRGARK 19

RESULT 11 FL3L_HUMAN

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TISSUE=T-cell;
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P26898;
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DOMAIN
TRANSMEM
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CARBOHYD
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IL2A_SHEEP
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        DORENT LEADER TO LEADER TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
DN-LINKED (GLCNAC. .) (POTENTIAL).
DSSTLEPPWSRRELEATA -> VETVFHRVSQDGLDLLTS
(IN ISOFORM 2).
(IN ISOFORM 2).
G -> A (IN ISOFORM 2).
G -> A (IN ISOFORM 2).
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MEDLINE=88212503; PubMed=2835311;
Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.,
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1nterleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                             SL CYTOKINE.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%; Score 36; DB 50.0%; Pred. No. 11;
     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                26416 MW;
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Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 CLHWORTRRR 213
                                                                                                                                                                                                                                                                                                                                                                                             235 AA;
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                                                                                                                                                                                                                                                                                     161
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                                                                                TRANSMEM
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DISULFID
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DISULFID
CARBOHYD
CARBOHYD
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A Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;

Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;

Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.;

Corporationing of a coby encoding the ovine interleukin-2 receptor 55-kDa (1925.);

Gene 113:283-284(1992).

Corporation: Roceptor For INTERLEUKIN-2.

CONTAIN: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH APPINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE (MITH A GAMMA CHAIN.)

CONTAIN: THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE (MITH A GAMMA CHAIN.)

CONTAINS: SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FNBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licensee.beb.chb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
11-FBB-1996 (Rel. 31) Last annotation update)
11nterleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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0
                                                                                                          Glycoprotein; Receptor; Repeat; Signal; Sushi.
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Pred. No. 13;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                        -LINKED (GLCNAC. . .) (P. 4901BBF9A4862390 CRC64;
                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AA
                                                                                                                                                                                                                                   SUSHI 1.
SUSHI 2.
PIR; SO7442; S07442.
HSSP; P01589; 11LM.
INCEPERO; IPRO00436; Sushi_SCR_CCP.
Efam; PF00084; sushi; 2.
SMART; SM00032; CCP; 2.
Transmembrane; Glycoprotein; Recept
                                                                                                                                                                                                                                                                                                                                                                                                          31238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CLIWORKWKKNR 272
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275 AA;
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Best Local Similarity
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Repeat; P
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AC 091702
DT 16-0CT
DT 16-0CT
DE POTENT
GN ATSC23
OC ENRATY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Tahlir M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 275-378 FROM N.A.
MEDLINE=97019052; PubMed=8865668;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enthartoideae, Oryzeae, Oryza.
                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SUSHI 1.
SUSHI 2.
BY SHILLARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINED (GLCNAC. . .) (POTENTIAL).
S -> T (IN REF. 2).
W, 1101AZDE5ACSA088 CRC64;
                                                                                                              Transmembrane; Glycoprotein; Receptor; Repeat; Signal; Sushi.
SIGNAL
1 21 BY SIMILARITY.
CHAIN 22 275 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
TRANSMEM 244 262 POTENTIAL.
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Pred. No. 13;
1; Mismatches 5; Indels
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PHYC.ORYSA STANDAML.
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
     EMBL; 211560; CAA77652.1; --
BMBL; X60149; CAA42723.1; --
BMBL; X19167; CAA42723.1; --
BML; X18910; S18910.
PIR; S18999; S18899.
PIR; JC1113; JC1113.
HSSP; PO1589; IIIM.
INTERPO; IRTOO0445; SUSHİ, SCR_CCP.
FMEM; PPO0084; SUSHİ, 2.
                                                                                                                                                                                                                                                                 30904 MW;
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275 AA;
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DISULFID
DISULFID
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DISULFID
CARBOHYD
CONFLICT
SEQUENCE
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PHYC ORYSA
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- STRUBUNIT: HOMODIMER (BY SIMILARITY).
-!- PIM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Q9LT02;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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824 PAS 2.

124 HISTIDINE KINASE.

322 CHROMOPHORE (BY SIMILARITY).

279 F - S (IN REF. 2).

5125982 MW, P2AS20181CFE7B32 CRC64;
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Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; ABO18442; BAA74448.1; -.
EMBL; U61207; ABA81996.1; -.
InterPro; IPR003594; APbind_ATPase.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004359; HIS_KIN sig.
InterPro; IPR001610; His_kinĀ.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS_domain.
InterPro; IPR001294; Phytochrome.
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36.4%;
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1137 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0119; CATATPASE.
PROSITE; PS00154; ATPASE_E1_E2; 1.
Mydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
                                                                                                                                                                                                "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                         SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                      POLY-LYS.
PHOSPHORYLATION (BY SIMILARITY).
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MAGNESIUM (BY SIMILARITY).
W; 4A3E82D2222A4D78 CRC64;
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nterbro, IRR001454, Hignase/hydrlase.
(Eam, PF00122, B1-E2 ATPase; 1.
(Eam, PF00702, Hydrolase, 1.
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Gaps

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Score 36; DB 1; Length 1179; Pred. No. 56; 3; Mismatches 2; Indels

Query Match
Best Local Similarity 44.4%;
Matches 4; Conservative

1 CFQWQRXMR 9

Db 1144 CYSWERLLR 1152

Search completed: February 21, 2003, 07:51:37 Job time : 5.2093 secs

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Qgeenz arabidopsis
O22188 arabidopsis
O22188 arabidopsis
O22188 arabidopsis
Qgews6 lycopersico
Qgws518 salmonella
Qgyqc0 human immun
Qgyqbb human immun
Qgyjij human immun
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Qgylan arabidopsis
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1-JUN-2002 (Human)
1-JUN-2002 (H
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human) (Fragment).
Bukaryota, Metazoa; Chordata; Craniata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 711 AA.
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09YJ17
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TISSUE=PROSTATE;
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Q9tcg0 ovyza saties
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Q19150 caenorhabdi
Q19153 caenorhabdi
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Q8460 rhizobium 1
Q9xtg zriccolium 1
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Q8xe2 ralstonia s
Q8xe2 ralstonia s
Q8xex2 homo sapien
Q77855 human immun
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114.078 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                          February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9TCY8
Q9XFD3
Q9X7B0
Q93780
Q93780
Q98CA0
Q8UHC2
Q8UHC2
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Q77855
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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SIGUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=ZOVA970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBL_TaxID=6239;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
genes that are differentially expressed at rice young panicle."; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1-SIMILARITY: BELONGS TO THE CYTOCHROWE P450 FAMILY.
EMBL; AF140486; AAD29699.1; -.
InterPro; IPRO01128; Cytochrome_P450.
Pfam; PF00067; P450.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
Heme: Monoxygenase; Oxidoređuctase.
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                                                                                                                                                                                                                                                                                                                                                                                        62.1%; Score 41; DB 10; Length 105; 60.0%; Pred. No. 2.3; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.6%; Score 40; DB 10; Length 148; 66,7%; Pred. No. 5.1; 1ve 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00499; AAI; 1.
SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                           SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
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Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F53H4 4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 148 AA.
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J. Agric. Food Chem. 47:4932-4938(1999).
EMBL; AF091841; AAD42943.1; -.
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InterPro; IPR00617; Napin.
InterPro; IPR001768; Try/amyl inhbtr.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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PRINTS; PR00496; NAPIN.
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Best Local Similarity 66.70,
Best aca 6, Conservative
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les 6; Conservative
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Caenorhabditis elegans.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P40 (Fragment).
Cytochrome P40 (Fragment).
Eukaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                      Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER TOWN (TEMBLE) 13, Created)
O1-MAY-2000 (TEMBLE) 13, Last sequence update)
O1-MAY-2000 (TEMBLE) 17, Last annotation update)
O1-JUN-2001 (TEMBLE) 17, Last annotation update)
Covis aries (Sheep).
Dikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bikaryota; Metazoa; Chordata; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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"Suppression subtractive hybridization (SSH) identified candidate
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   Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                               83.3%; Score 55; DB 4; Length 38; 90.9%; Pred. No. 0.0019; ive 0; Mismatches 1; Indels
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MEDLINE=95127729; PubMed=7827104;
MEDLINE=95127729; PubMed=7827104;
Bidan Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. 210phys. Acta 1243:25-32 (1995).
HSSP, 077698; 1CEZ.
InterPro; IPRO01156; Transferrin.
Pfam; PPRO0405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                InterPro; IPR0011156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402P490B5EBDDEB CRC64;
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                                                                                     SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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les 7; Conservative
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TISSUE=PANICLE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORXMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 CFHWKSLRROVR 99
                                                                                                                                                                                                                                                                                                       Mesorhizobium loti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=176299;
                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome SEQUENCE 205 AA
                                                                                                                                             NCBI_TaxID=381;
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                                                                                                              Score 40; DB 5; Length 275;
Pred. No. 9.7;
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                                                                                                                                                                                                                           3; Indels
                       Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, 1050309; AAG24025.1;
INTERPO, IRRO00731; HMGCR/patch_STM.
PROSITE; PS50156; SSD; 1.
                                                                                                     "Genome sequence of the nematode C.elegans: A platform investigating biology."; Science 282:2012-2018[198]. EMBL; 281089; CAB03137.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
Favello A., Gattung S.;
"The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDSJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 932 AA; 105144 MM; 66680619ADACBFDS CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 20, Last annotation update)
Hypotherical 105.1 kba protein.
F07C3.1.
                                                                                                                                                                                   60.6%; Scor.
63.6%; Pred. No. y...
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                                                 [2]
SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ERISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.0.
                                                                                                                                                                                        Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                 262 FÓWKISMRKTR 272
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                                                                                                                                                                                                                                                      2 FOWORXMEKVR 12
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SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Waterston R.;
       SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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STRAIN=MAPF303099;
MEDLINE=21082930; PubMed=11214968;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Bisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley P., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V., Nester E.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                           Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyridoxamine 5'-phosphate oxidase.

PDXH OR ATU0760 OR AGR C 1381.
Agrobacterium tumefaciene (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
01-OCT-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 16, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBUNC2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:331-338(2000).
EMBL, AP003011; BAB53553.1; - .
InterPror; IRRO0655; Pyridox.oxidase.
Pfam; PF01243; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox oxidase; 1.
IIGRFAMs; TIGR00558; pdxH; 1.
PROSITE; PS01064; PYRIDOX OXIDASE; 1.
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MEDLINE=21608551; PubMed=11743194;
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us-09-743-107b-90.rspt

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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

REALNISHMA ATCC 23456 / BIOTYPE 1;

RX MEDLINE=20020109; Pubmed=11756688;

RA JUBOURN, Anderson I., Bhattachartya A., Lykidis A., Reznik G.,

RA JUBOURN, L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

RA JUBOURN, L., Larsen N., Overbeek R.;

RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

RA Haselkorn R., Kyrpides N., Overbeek R.;

RT Hre genome sequence of the facultative intracellular pathogen

RT Brucella melitensis.";

RT Brucella melitensis.";

RT BRO05587; AAL52698.1;

DR EMBL, ABC09587; AAL52698.1;

DR InterPro; IPR00659; Pyridox_oxidase.

ProDom; PO06512; Pyridox_oxidase;

ProDom; PO06512; Pyridox_oxidase;

RT GRPAMS; TIGRO0558; pdxH;

DR ProDom; PO06512; Pyridox_oxidase;

RW Oxidoreductase; Complete Proteone.

SEQUENCE 208 AA; 23866 NW; CBIF50BC9612DE28 CRC64;
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MEDLINE=21681879; PubMed=11823852;
Salanoubar M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Mature 415:497-602(2002)
                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella
NCBI_TaxID=29459;
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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        01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
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Pred. No. 11;
2; Mismatches
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InterPro; IPR004844; S/T phosphtse.
Pfam; PF00149; Metallophos; 1.
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SEQUENCE 279 AA; 31541
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Best Local Similarity 50...
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                                                                                    Brucella melitensis.
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Best Local Similarity
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Q8XSE2
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WEDLINE=2195650; PubMed=11481430;

GTRAIN=1021;

MEDLINE=2195650; PubMed=11481430;

MEDLINE=2195650; PubMed=11481430;

A Gapela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,

B Goistard P., Becker A., Boutry M., Cadieu B., Dreano S., Gloux S.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maeuy D.,

A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Maeuy D.,

B Hant C., Thebault P., Puehler A., Purnelle B., Ramsperger U.,

R Renard C., Thebault P., Puehler A., Purnelle B., Ramsperger U.,

R Ranalysis of the chromosome sequence of the legume symbiont

T. Analysis of the chromosome sequence of the legume symbiont

Proc. Natl. Acad. Sci. U.S. 98:9877-9882 (2001).

EMBL; AL591785; CAC45467.1; -..

EMBL; AL591785; CAC45467.1; -..

Proc. Natl. Acad. Sci. U.S. 98:9877-9882 (2001).

R HEND: AL591785; CAC45467.1; -..

Probom; PRO006312; Pyridox oxidase.

Probom; PRO006312; Pyridox oxidase.

Probom; PRO006312; Pyridox oxidase; I.

TIGRNOSTIE; PSO1064; PRRIDOX_OXIDASE; UNKNOWN_I.
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmtel K., Gordon J., Vaudin M., Iartchouk O., Epp. A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Growell C., Gurson J., Lomo C., Sear C., Strub G.,
Gelo C., Slater S.,
Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
Science 294:2322-2328(2001).
EMBL; AE009043; AAL41776.1; -.
EMBL; AE008009; AAK86569.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
(EC 1.4.3.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                   59.1%; Score 39; DB 16; Length 206; 50.0%; Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Complete proteome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
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Last sequence update)
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01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity
Matches 6; Conserv
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es 6; Conserv
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Q92RH8

RESULT 10 Q92RH8

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Best Loca Matches

OBYFK3

RESULT 11 Q8YFK3

88

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Search completed: February 21, 2003, 08:00:44 Job time : 22.6744 secs
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NON TER
SEQUENCE
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Q77855;
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TESCUELE FROM N.A.

A Nishikawa T., Nagaik K., Sugiyama T., Otsuki T., Suzuki Y.,

A Nishikawa T., Nagaik K., Sugano S., Shiratori A., Sudo H.,

A Mishikawa T., Nagaik K., Sugano S., Shiratori A., Sudo H.,

A Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

A Matanabah M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

A Matanaba S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

A Manomoto J., Wakamatay A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.,

I'm WEDO Muman cDNA sequencing project.",

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK002037; BAA92048.1; -..

SEMEL; AK002037; BAA92048.1; -..

RICEPPO; IPR000008; C2.

InterPro; IPR000008; C2.

RICEPPO; IPR00160; C2.

RICEPPO; IPR00160; C2.

REMEL; SR00160; C2.

REMART; SR00239; C2. IOWAIN 1; UNKNOWN 1.

REMART; SR0049; C2. DOWAIN 2; 1.

RECSITE; PS00030; RRM RNP 1; UNKNOWN 1.

RECSITE; PS00030; RRM RNP 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 21, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacylglycerol-binding protein UNC-13.
HOMO saplens (Human).
Eukaryota; Metazos; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 59.1%; Score 39; DB 4; Length 306; Best Local Similarity 55.6%; Pred. No. 17; Matches 5; Conservative 2; Mismatches 2; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025/08. BAH25708.1; -. Hypothetical protein. SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 AA
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                                                                                                                                                                                                          PRELIMINARY;
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                                                        244 CFÓWEKGTRTAK 255
1 CFOWORXMRKVR 12
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TISSUE=PANCREAS;
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Q9NUS2;
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28TAX2
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J. Virol. 69:2285-2296(1995).

J. Virol. 69:2285-2296(1995).

J. Pfam, PRODS16; GP120.

Pfam, PRODS16; GP120.

Pfam, PRODS16; GP120.

Pfam, PRODS16; GP120.
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   DB 4; Length 466;
                                                          2; Indels
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                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                     91 AA.
59.1%; Score 39; DB 55.6%; Pred. No. 26; iive 2; Mismatches
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Query Match
Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                     269 CFÓWESTLR 277
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67 QWNRTLQKVR 76
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Human lactoferrin

Human lactoferrin
Peptide for anti-u
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
Human lactoferrin
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Human lactoferrin

Advanced glycosyla Human lactoferrin Amino acid sequenc Human lactoferrin Anti microbial pep Lactoferrin-relate

Lactoferrin derive Lactoferrin derive Lactoferrin derive Lactoferrin derive Bovine lactoferrin

Anti-parasitic lac Anti-parasitic lac Peptide for anti-u Lactoferrin-derive Lactoferrin-derive Lactoferrin derive

Lactoferrin-derive Lactoferrin-derive Lactoferrin deriva Anti-parasitic pep

Dolphin GT;

Result No.

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Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
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AAR84698
AAR84699
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AAR87622
AAW26150
AAW14036
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AAR80264
AAR98553
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AAW03045
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AAW13397
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AAR21810
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                                   AAY78035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002441.
98SE-0002562.
98SE-0004614.
99WO-SE01230
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Human lactoferrin
Human lactoferrin
Human lactoferrin
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Human lactoferrin
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Human lactoferrin
Human lactoferrin
Human lactoferrin
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Human lactoferrin
Human lactoferrin
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                                                                                 ; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                   A Geneseq 101002:*

| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
| SIDS2/gcgdata/geneseq-emb1/AA1981.DAT:*
| SIDS2/gcgdata/geneseq-emb1/AA1981.DAT:*
| SIDS2/gcgdata/geneseq-emb1/AA1981.DAT:*
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| SIDS2/gcgdata/geneseq-emb1/AA1991.DAT:*
| SIDS2/gcgdata/geneseq-geneseqp-emb1/AA1991.DAT:*
| SIDS2/gcgdata/geneseqg-geneseqp-emb1/AA1991.DAT:*
| SIDS2/gcgdata/geneseqg-geneseqg-emb1/AA1991.DAT:*
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| SIDS2/gcgdata/geneseqg-geneseqg-emb1/AA1991.DAT:*
| SIDS2/gcgdata/geneseqg-geneseqg-emb1/AA1991.DAT:*
| SIDS2/gcgdata/geneseqg-gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
        5.1.3
Compugen Ltd.
                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                             908470 seqs, 133250620 residues
         GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                  February 21, 2003, 07:37:21
                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                         OM protein - protein search, using sw model
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AAY78092
AAY78038
AAY78046
AAY78046
AAY78081
AAY780908
AAY780908
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Gapop 10.0 , Gapext 0.5
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71
1 CFQWKRNMRKVR 12
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Perfect score:
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71
67
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all inicially on a broad basis because of high production costs. Therefore, provision of peptides because of high production enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 71; DB 21; Length 12; Best Local Similarity 100.0%; Pred. No. 2.1e-05; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:92.
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                                                                   Claim 22; Page 38; 102pp; English.
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98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                             12 AA;
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29-DEC-1998;
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AAY78092
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment our inary tract infections, colitis, and Candida infections (such as membrane) inflammations, colitis, and Candida infection on a meuosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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98SE-0004614.
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Best Local Similarity 100.
Matches 12; Conservative
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17-JUL-1998;
29-DEC-1998;
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Homo sapiens.
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Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used allinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tun
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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98SE-0002562.
98SE-0004614.
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Matches 11; Conserv
                                                                                                                                      12 AA;
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as urinary tract infearing and/or prevention of infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also functioned and bactericidal and may also be used as preservatives.

Seven though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides because of high production costs. Therefore, provision of peptides based on lactoferrin would
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                     DB 21; hens.
9.7e-05; Indels
                                                                Length 12;
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                                                       Score 67; DB 2
Pred. No. 9.7e-
1; Mismatches
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98SE-0002562.
98SE-0004614.
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91.7%;
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hes 11; Conservative
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Best Local Similarity
Matches 11; Conserv
12 AA;
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17-JUL-1998;
29-DEC-1998;
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AAY78037 standard; Peptide; 13 AA.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                                                                                                food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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                                                                                                               AAY78084 standard; Peptide; 12 AA.
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91.78;
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98SE-0002562.
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Best Local Similarity 91.7
Matches 11, Conservative
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              1 CFQWQRNMRKVR 12
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17-JUL-1998;
29-DEC-1998;
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                                                                             RESULT 6
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumoure. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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                                                                                                                 Human, lactoferrin, modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 0.00011;
1; Mismatches 0; Indels
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                                                                                        Human lactoferrin derived peptide SEQ ID NO:37,
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98SE-0002562.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or intensy tract infections. A medicinal product of the peptide or fragment or interview the circulation and/or prevention of infections (such as unconsultinary inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fundicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anth-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
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Matches 11, Conservative
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                                                                                                                                                                        Homo sapiens
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17-JUL-1998;
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                                                                                                                                                                                                     Synthetic.
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Dolphin GT,

Baltzer L,

Score 67; DB 21; Length 13; Pred. No. 0.00011; 1; Mismatches 0; Indels

94.4%;

Homo sapiens

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the burdent and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used for treating and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides can also be used as preservatives. Then though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.00011; .
1; Mismatches 0; Indels
                                                                                                                                                                                                            Dolphin GT
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                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                                                                                                                 Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%;
                                                                                                                                98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA;
                            WO200001730-A1.
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through the intestine lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, colitis, and candida infections (such as unihary tract inferences, colitis, and candida infections (such as unimary tract inferences, colitis, and candida infections a usodal infections and/or tumours. The peptides can also be used in the peptides are also fungicidal and bactericidal and may also be used as preservatives.

Breat chough native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.00011;
L; Mismatches 0; Indels
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                                                                                                            Baltzer L,
                                                                                                                                                                                                                            Claim 12; Page 69; 102pp; English.
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98SE-0002562.
98SE-0004614.
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91.7%;
                            98SE-0002562.
98SE-0004614.
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              98SE-0002441
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Best Local Similarity
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17-JUL-1998;
29-DEC-1998;
            06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                                              Hanson LA,
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Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                              New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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                                                                                                                Claim 15; Page 75; 102pp; English
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les 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
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17-JUL-1998;
29-DEC-1998;
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Hanson LA,
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0; Gaps

Claim 18; Page 75; 102pp; English

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infections (such as uninections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungacidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67; DB 21; Length 14; Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - has low toxicity, is
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heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MORG ) MORINAGA MILK IND CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       14 AA;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fundicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                    Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                     food, infant formula, anti-inflammatory, anti-microbial, anti-tum
urinary tract infection, colitis, Candida infection, fungicidal,
bactericidal, preservative.
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                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:35.
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                  AAY78035 standard; Peptide; 15 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                 25-APR-2000
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Matches
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AAY78035
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Human lactoferrin derived peptide SEQ ID NO:62.
25-APR-2000 (first entry)
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Dolphin GT

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment oan be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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98SE-0002562.
98SE-0004614.
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17-JUL-1998;
29-DEC-1998;
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Query Match 94.4%; Score 67; DB 21; Length 15; Best Local Similarity 91.7%; Pred. No. 0.00012; Matches 11; Conservative 1; Mismatches 0; Indels Sequence 15 AA;

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1 CFQWKRNMRKVR 12

4 CFQWQRNMRKVR 15

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Search completed: February 21, 2003, 07:56:44 Job time : 29.093 secs

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GENERAL INVERSION

APPLICANT: NARASHIMA, HIDEKI

APPLICANT: NARASHIMA, HIDEKI

APPLICANT: NARASHIMA, SHIGERAI

APPLICANT: TANAKA, SHIGERAI

APPLICANT: TANAKA, SHUN'ICHI

APPLICANT: TANAKA, SHUN'ICHI

APPLICANT: TOSHIDA, TOSHIMRO

APPLICANT: VINEBITINO: VIRAL INFECTION AND PROLIFERATION

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 8

CORRESSEDE: PATERY ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT

STREET: 53 STATE STREET

GITY: BOSTON

CONTRIBUTION

CONTRIBUTION

STREET: 53 STATE STREET
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LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
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ZIP: 02109
COMPUTER EDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBEL: PAULA A.
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: 32,503
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REGISTRATION NUMBER: 32,503
REGISTRATION OF SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TURNOTH AND ACTERISTICS:
LENGTH: 18 amino acids
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US-09-421-632-2
US-09-421-632-2
US-08-655-640-2
US-08-154-0319-4
US-08-161-0319-4
US-08-461-313-4
US-08-461-167-4
US-08-468-167-4
US-08-456-167-4
US-08-456-167-4
US-08-456-167-4
US-08-456-106-2
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US-09-265-577-2
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Patent No. 5565425
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MOLECULE TYPE: peptide
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US-08-204-487-3
6
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                     February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 1
Sequence 2
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5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-254-487-1
US-08-256-771-254
US-08-256-771-254
US-08-311-984-25
US-08-734-4
US-09-508-734-4
US-95-508-734-6
US-95-508-734-6
US-07-55-161A-10
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US-08-475-055-8
US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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71
1 CFQWKRNMRKVR 12
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Perfect score:
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No.
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94.4%;
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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Matches 11; Conserv
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FRAGMENT TYPE:
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US-08-475-055-8
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December 9, 408-101-1016/08465948
Perent No. 585582
GENERAL INFORMATION:
PAPLICANT: PHELEN VLASSARA
PAPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: EMPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES 9
CORRESPONDENCE ADDRESS:
PORRESPONDENCE ADDRESS:
STATE: ALL Hackensack Avenue
STREET: ALL Hackensack Avenue
CITY: Hackensack Avenue
STREET: ALL Hackensack Avenue
STREET: ALL Hackensack Avenue
CITY: Backensack Avenue
STREET: ALL Hackensack Avenue
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                                                                                          Query Match 94.4%; Score 67; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 9.9e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 18;
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; OTHER INFORMATION: (20-37)"
US-08-204-487-3
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Best Local Similarity 91.7%;
Matches 11; Conservative
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TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                    1 CFQWQRNMRKVR 12
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CFOWORINMRKVR 12

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PRESENT. INFORMATION:

PRESENT. INFORMATION:

APPLICANT: U.L. YONG MINO
APPLICANT: U.L. YONG MINO
APPLICANT: U.L. YONG MINO
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APPLICANT: MACHINE AND APPLICANT
STATE: MACHINE AND APPLICANT
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Query Match
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94.4%; Score 67; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 1; Mismatches 0. Thanh
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Sequence 3, Application US/07755161A
Fatent No. 5304633
Fatent No. 5304633
Fatent No. 5304633
Fatent No. 5304633
Fatent INCOMMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,217
FILING DATE:
APPLICATION NUMBER: 08/486,217
FILING DATE: APPLICATION
ATTORNEY/AGRAT INFORMATION:
ATTORNEY/AGRAT INFORMATION:
NAME: Jackson Eqq. David A.
REGISTRATION NUMBER: 947-1-008A
FILING DATE: APPLICATION:
ATTORNEY/AGRAT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID OS
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acide
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
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Length 20;

DB 1;

94.4%; Score 67;

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NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: 10
CHER INFORMATION: Cyg residue at location 19 connected by disulfide bond with
PUBLICATION: thiol group of Cyg residue at location 2"
AUTHORS.
AUTHORS.
                                       Inote= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YARAHMOTO, NAOKI
APPLICANT: YARAHMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: KAWASKI, YOSHIHIRO
APPLICANT: VAWASKI, YOSHIHIRO
APPLICANT: UNUMINA, TOSHIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
VINGER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.4%; Score 67; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 1; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STALE.

COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PARENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
TTING DATE: 02-WAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                    ) DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // Sequence 1, Application US/08204487
// Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-WAR-19794
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/COCKET UMBER: FJN.
TELECOMMINICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,503
                  IDENTIFICATION METHOD:
OTHER INFORMATION: Cys
OTHER INFORMATION: Cys
OTHER INFORMATION: thic
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Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                                                       Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: BOS Fifteenth Street, N.W., #700
STATE: D.C.
COUNTRY: U.S.A.
ZIP: ZOOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OMPUTER: DisplayWitte
COMPUTER: DisplayWitte
OMPUTER: DisplayWitte
COMPUTER: DisplayWitte
OMPUTER: DisplayWitte
COMPUTER: DisplayWitte
SOFTWARE DISPLAYFING:
FILING DATE: 2-MAY-1992
FILING DATE: 0-S-MAY-1992
FILING DATE: 0-S-MAY-1991
FILING DATE: 0-S-MAY-1991
FILING DATE: 0-S-MAY-1991
FILING DATE: 0-S-SEP-1991
ATPORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek Jr.
REGIGTRATION NUMBER: 33, 367
PROPERTY NUMBER: 33, 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELENCOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
WATTS:
FEATURE:
NAME/KEY: modified site
  91.78;
Best Local Similarity 91.7
Matches 11, Conservative
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DEVELOPMENTAL STAGE
HAPLOTYPE:
                                                                 1 CFQWKRNMRKVR 12
                                                                                        2 CFQWQRNMRKVR 13
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE;
                                                                                                                                                                                            US-07-891-174-3
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STRANDEDNESS:
                                                                                                                                                                                                                                                      RESULT 9
US-08-256-771-25
              US-08-256-771-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-08-381-984-24
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Sequence 24, Application US/08256771

Sequence 24, Application US/08256771

Sequence 24, Application US/08256771

Fatent No. 565591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBLAL ACENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCS ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                         Query Match 94.4%; Score 67; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 1; Mismatches 0; Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                 /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: TIEM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771 FILING DATE: July 22, 1994 CLASSIFICATION 514 PRIOR APPLICATION DATA:
APPLICATION NUMBER: END STRICK DATE: APPLICATION NUMBER: FILING DATE: RILING DATE: FILING DATE: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TRLECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid stranbedness: single
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: peptide

FAAURE:
NAME/KEY: Peptide

LOCATION: 1.20

OTHER INFORMATION: /not;

GC-08-204-487-1
                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
TELEX:
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                                                                                                                                                                                                                                            Sequence 25, Application US/08256771
Fatent No. 5556591
GENERAL INCOMATION TOMITA et al.
TITLE OF INVENTION: PRODUCTS THEREWITH
ITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES. 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: 0.C.
STREET: 0.C.
STREET: 0.C.
STREET: 0.C.
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                                                  Gaps
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US-08-256-771-25
    94.4%; Score 67; DB 1; Length 20; 91.7%; Pred. No. 0.00011; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.4%; Score 67; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM COMPUTER: SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: JALY 22, 1994 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: WARTEN, T. Cheek, Jr. REGISTRATION NUMBER: 33,36 REFERENCE/DOCKET NUMBER:
Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                      1 CFQWKRNMRKVR 12
                                                                                                                2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWKRNIMRKVR 12
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
FILE REFERENCE: PA/SYG/00139
CURRENT PRILICATION WUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%; Score 67; DB 1; Length 20; 91.7%; Pred. No. 0.00011; ive 1; Mismatches 0; Indels
                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: DISKETTE, 1.44 mb
COMPUTER: DISKETTE, 1.44 mb
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                  805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-508-734-4
; Secuence 4, Application US/09508734
; Patent No. 64, 253509
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWKRNMRKVR 12
                                                                                  STREET: 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: siz
                                                                                                                                                             U.S.A.
                                                                                                                                                                               20005
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                                                                                                                                                               COUNTRY:
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LOCATION:
LOCATION:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
; Sequence 24, Application US/08381984
; Patent No. 5804555
; GRNEAL INFORMATION:
; TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Weahington
STATE: D.C.
COUNTY: U.S.A.
ZIP: 20055
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIPCATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/08381984
Patent No. 5804555
GANERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NIWBER:
REFFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWAY TO STAIL ON:

UNITS:

UNITS:

WANDE/KES:

LOCATION: 4

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of

OTHER INFORMATION: Chiol group of

OTHER INFORMATION: Chiol group of cys residue at location 4 connected by disulfide bond with

OTHER INFORMATION: thiol group of Cys residue at location 21"

RAME/KES: modified site

LOCATION: 21

IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                              REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
IENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWKRNMRKVR 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
MMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: HYPOTHETICAL:
        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11,
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                          ö
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                          Ouery Match 94.4%; Score 67; DB 4; Length 22; Best Local Similarity 91.7%; Pred. No. 0.00012; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.4%; Score 67; DB 4; Length 24; Best Local Similarity 91.7%; Pred. No. 0.00013; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-07-755-161A-10

Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, SOOKD

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: SYSTEM: MS-DOS

COMPUTER: DISKSTEM: MS-DOS

COMPUTER: DISKSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
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PRIOR APPLICATION DATA;
APPLICATION NUMBER;
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                    1 CFOWKRIMRKVR 12
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LENGTH: 24
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Gaps . 0

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IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 94.4%; Score 67; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 0.00013; Matches 11; Conservative 1; Mismatches 0; Indels
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FILING DATE:
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RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
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JOURNAL:
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TELEX:
INFORMATION FOR SED ID NO: 10:
SEGURANCE CHRACTERISTICS:
LENGTH: 25 amino acid
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T
                                                       DESCRIPTION:

Sequent No. 5317084

Batent No. 5317084

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

Antimicrobial Peptides and an TITLE OF INVENTION:

Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Wanderoth, Lind & Ponack
STRET: 805 Fifteenth Street, N.W., #700

STRET: B.C.

COUNTRY: U.S.A.

ZIP: 2005

COMPUTER READABLE FORM:

MEDIUM TYPE: DisplayWite

COMPUTER: IBM Compatible
OPERATION STREE: DisplayWite

COMPUTER: DisplayWite

COMPUTER: DisplayWite

COMPUTER: DisplayWite

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,367

REDERBONG/DOCKET NUMBER:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,367

RELECOMMUNICATION INFORMATION:

TELECHOMMUNICATION INFORMATION:

TELECHOME: 202-371-8856
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Sequence

Sequence 119, Appl Sequence 14, Appl Sequence 24, Appl Sequence 28, Appl Sequence 30, Appl Sequence 11, Appl Sequence 11, Appl Sequence 18, Appl Sequence 38, Appl

Sequence 194, App Sequence 4, Appli

Sequence 12129, *1* Sequence 13026, *1* 

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94.4%; Score 67; DB 9; Length 15; 91.7%; Pred. No. 5.1e-05; tive 1; Mismatches 0; Indels
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US-09-815-242-13026
US-09-879-957-194
US-09-978-697-119
US-09-978-119
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US-09-978-119
US-09-916-119
US-09-916-49A-6
US-09-916-49A-24
US-09-916-49A-24
US-09-916-49A-30
US-09-916-49A-30
US-09-916-49A-30
US-09-916-49A-32
US-09-916-49A-38
US-09-98-649A-38
US-10-028-98-38
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: ASLUR SVETNBJ (RNSSON
APPLICANT: LARS VORLAND
ITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFRERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: CO1-02-77
PRIOR PELING DATE: 2001-02-77
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1998-08-31
SEQIENCE: PRESENENCE OF SEQIENCES: SOFTWARE: PRESENENCES: SEQIENCES: SEQUENCES: SEQUE
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APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
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      TYPE: PRT
ORGANISM: HOMO SAPIENS
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Matches
      Sequence 20, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 2, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 47985, Aspl
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Sequence 5715, Ap
Sequence 1248, Ap
Sequence 119, App
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54.162 Million cell updates/sec
                                                                                                                                                                                                            February 21, 2003, 08:08:15 ; Search time 6.88372 Seconds
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cgn2_6/ptodate/2/pubpaa/USOB NEW PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_NEW_PUB.pep:*

cgn2_6/ptodate/2/pubpaa/USOB_PUBCOMB.pep:*

                              GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-888-320-2
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US-09-798-869-20
US-00-62-966-2
US-09-798-869-3
US-09-798-869-3
US-09-798-869-3
US-09-798-869-4
US-09-798-869-4
US-09-798-869-4
US-09-798-869-8
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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71
1 CFQWKRNMRKVR 12
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Gaps

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Query Match 94.4%; Score 67; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.0017; Matches 11; Conservative 1; Mismatches 0; Indels
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83.1%; Score 59; DB 9; Length 15;
Best Local Similarity 83.3%; Pred. No. 0.001;
Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                       RESULT 4

US-09-798-869-6

US-09-798-869-6

Sequence 6, Application US/09798869

Fublication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT:
:
BIOGATIVE PEPTIDES
FILE REFRENCE:
A34049-PCT-USA-A

CURRANT FILING DATE:
CURRANT FILING DATE:
PRIOR PLING DATE:
PRIOR PLING DATE:
PRIOR PLING DATE:
APPLICANTON NUMBER:
BRIOR PLING DATE:
ANUMBER OF SEQ ID NOS:
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JOS-09-798-80-3

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JOS-08-10-1

JOSERAL INFORMATION

JAPLICANT: JOSH SIGURD SVENDEN

APPLICANT: JOSH SIGURD SVENDEN

APPLICANT: JAKS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION BIOACTIVE PEPTIDES

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT PILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: GG1899/02851

PRIOR APPLICATION NUMBER: GG1899/02851

PRIOR APPLICATION NUMBER: G89818938.4

PRIOR FILING DATE: 1998-08-31

PRIOR FILING DATE: 1998-08-31

PRIOR FILING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SEQ ID NO 3

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Best Local Similarity
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US-09-798-869-3
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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 67; DB 9; Length 25;
Pred. No. 8.2e-05;
1; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25.
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE DOCKET NUMBER: 31,409
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 638-6666
                             FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-34
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRACKE OF WINDOWS VERSION 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 94.4%;
1 Similarity 91.7%;
11; Conservative 1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-10-023-096-2
       LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo Sapiens
US-09-798-869-20
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Best Local Similarity
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54.5%; Pred. No. 1.3;
ive 2; Mismatches
                                                                                                                                                                                                  PEDICACTION US/09798869
PUBLICACTION US/09798869
PUBLICACTION US/0902821A1
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVENBAL
APPLICANT: BALDUR SVENBAL
APPLICANT: LARS VORLAND
TITLE REPERBNCE: A34049-PCT-USA-A
CURRENT RILLAND DATE: 2001-02-27
CURRENT RILLOR DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PGT/GB99/02861
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARR: FABELSEQ for Windows Version 4.0
SERVICTH: 15
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Matches 6, Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
         CPQWKRNMRKV 11
                                                           CYÓWOWRMRKL 13
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CRGANISM: MURINE
US-09-798-869-4
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         Gaps
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      1; Indels
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Pred. No. 0.045;
                                                                                                                                                                                                                     3; Mismatches
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PUBLICATION NO. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACITUE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB8818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
SSOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.0.
7; Conservative
                                                           CFOWKRNMRKV 11
                                                                                                                 CYQWQRRMRKL 13
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US-09-798-869-23
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Matches
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Pred. No. 2.4;
4; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                  TITE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1099-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USOURCE 29, Application US/09798869
Sequence 29, Application US/09798869
PUBLICATION NO. USZ030022281A1
SERREAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN RENDAL
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILE OF INVENTION BIOACTIVE PEPTIDES
TILE REPERRINCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOPTHARE: PRACES PRACEON NUMBER: PCT/GB99/02851
NUMBER OF SEQ ID NOS: 30
                                                                                                                                                                      Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN ERCAL
APPLICANT: BALDIR SYGINDS (NSSON)
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 45.5
Matches 5, Conservative
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                               CYGWKRNNKGV 58
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1 CFQWKRNMRKV 11
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US-09-798-869-29
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LENGTH: 15
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Pred. No. 29;
2; Mismatches 3; Indels
           | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 10 | Sequence | 1
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Best Local Similarity 54.5
Matches 6; Conservative
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US-09-796-753-26
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LENGTH: 333
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GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: Barry III, Clifton E.
APPLICANT: Maluli, Khisimuzi
APPLICANT: Maluli, Khisimuzi
APPLICANT: Bekker, Linda-Gail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN B1474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
US-09-864-761-47985
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                                                          PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARR: Aniomax Sequence Listing Engine vers: 1.1
SEQ ID NO 47985
   APPLICATION NUMBER: PCT/US01/00663
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Publication No. US20030013090A1
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ORGANISM: Homo sapiens
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16 CFOWRR 21
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Sequence 47985, Application US/09864761
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wenskeng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRIOR DATE: 2000-05-26
PRIOR PLING DATE: 2000-06-26
PRIOR PLING DATE: 2000-09-27
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PRIOR PLING DATE: 2001-03-30
PRIOR PLING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00664
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR APPLICATION NUMBER: PCT/USO1/00669
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Pred. No. 2.4;
4; Mismatches
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APPLICANT: (YSTEIN REDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00668
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APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
                                                                                                     RESULT 13
JS-09-798-869-30
JS-09-798-869-30
Sequence 30, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                  Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
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Best Local Similarity 45.5
Matches 5; Conservative
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3 CFRWQWRMKKL 13
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ORGANISM: BOVINE
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Search completed: February 21, 2003, 08:11:56 Job time : 6.88372 secs

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                                                                    February 21, 2003, 07:48:01 ; Search time 10.6047 Seconds
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                   283224 segs, 96134422 residues
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                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Match Length DB
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
Sequence:
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hypothetical prote	GTP-binding regula	hypothetical prote	trichohyalin like	hypothetical prote	hypothetical prote	F15I1.22 [imported	hypothetical prote	60S ribosomal prot	hypothetical prote	pre-pilin leader p	33.3K hypothetical	hypothetical prote	hypothetical prote	MHC class I histoc	pectate lyase (EC
T17324	S52418	T28820	B85431	AC1714	AG1343	C96582	H81246	T00407	G98020	E82546	G86403	T16882	T29571	137477	WZWCPC
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37	37	37	37	36	36				36						
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Richo, Y.

Submitted to the EMBL Data Library, March 1994
A; Reference number: 606820
A; Accession: G01394
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-711 ACHO
A; Cross-references: EMBL: U00643; NID: 9467236; PIDN: AAB60324.1; PID: 9467237
B; Rey, M. W.; Waloshuw; S. L.; deBoer, H.A.; Pieper, P.R.
Nucleic Acids Res. 18, 5288, 1990
A; Tile: Complete nucleoride sequence of human mammary gland lactoferrin.
A; Reference number: 311228
A; Accession: S1128
A; Molecule type: mRNA
A; Residues: 1-148, "T', 150-422, "C', 424-711 AREY>
A; Residues: EMBL: X53961; NID: 934415; PIDN: CAA37914.1; PID: 934416
B; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol: 6, 1969-1981, 1992
A; Ritte: Differential molecular mechanism of the estrogen action that regulates lactofes and accession. Ascession. 
                                                                                                                                                                                                                                                                                                                                                                                                                        N,Alternate names: lactoferrin
C.Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S7
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R)Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A,Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A,Reference number: S15853; MUID:91264786; PMID:2049066
A)Accession: S15853
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
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A,Residues: 1-15 <TEN>
A,Residues: 1-15 <TEN>
A,Residues: 1-15 <TEN>
A,COSENECATE GESSESS9; NID:g263311; PIDN:AAB24877.1; PID:g263312
A,Experimental source: placenta
A,Rote: sequence extracted from NCBI backbone (NCBIP:122202)
R,Powell, M.J.; Ogden, J.E.
Nucleic, Acids Res. 18, 4013, 1990
A,Title: Nucleotide sequence of human lactoferrin cDNA.
A,Title: Nucleotide sequence of human lactoferrin cDNA.
A,Reference number: $10324; MUID:90326549; PMID:2374734
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                      lactotransferrin precursor [validated] - human
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A;Molecule type: mRNA
A;Residues: 3-711 <POW>
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A, Molecule type: protein A, Residues: 20-28, 'X', 30-31 <ST2>

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A; Accession: S20841

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pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (st
C;Species: Agrobacterium tumefaciens
C;Date: 30.58p-2001 #sequence_revision 30.58p-2001 #text_change 11-Jan-2002
C;Accession: H97451
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Ovis crientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S22107
Biochim. Biophys. Acta 1243, 25-32 1995
A;Title: Isolabiton and characterization of sheep lactoferrin, an inhibitor of platelet
A;Reference number: S52107; MUID:95127729; PMID:7627104
A;Accession: S52107
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A;Residues: 1-275 <WIL>
A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F53H4.4 - Caenorhabditis elegans
C.Speciese Caenorhabditis elegans
C.Speciese 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Accession: T22597
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A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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                                          Length 708
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A,Molecule type: protein
A,Residues: 1-33 <QIA>
C;Superfamily: transferrin, transferrin repeat homology
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                                                                                                                                    3; Mismatches
                                               70.4%;
                                               Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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262 FQWKISMRKTR 272
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Matches 6; Conserv
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Matches 8; Conserv
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A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; transferrin spredicted <51G>
F;1-19/Domain: signal sequence #status predicted <51G>
F;20-711/Product: lactotransferrin repeat homology <TRH1>
F;20-699/Domain: transferrin repeat homology <TRH2>
F;20-659/Domain: transferrin repeat homology <TRH2>
F;20-65,39-66,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status eF;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #status
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A;Residues: 436-487,'A',489-711 <RAD>
A;Residues: 436-487,'A',489-711 <RAD>
A;Residues: 436-487,'A', 489-711 <RAD>
A;Croser references: Balb:MB642; NID:9168815; PIDN:AAA86665.1; PID:9386855
R;Panella, T.U.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Ttflerence number: A61169; MUID:91235214; PMID:1674448
A;Reference number: A61169; MUID:91235214; PMID:1674448
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'Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

'Note: this is the final paper in a series

'Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

ur. J. Blochem. 241, 303-308, 1996

'Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin

'Reference number: S74119, MUID:97054624; PMID:8898921
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Blochem, Blopkye, Res. Commun. 203, 1344-1332, 1994
A/Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: JC2323; MUID:94380047; PMID:8093048
;Rado, T.A.; Wei, X.; Benz Jr., E.J.
lood 70, 989-993, 1987
;Title: Isolation of lactoferrin cDNA from a human'myeloid library and expression of
;Reference number: S07160; WUID:88001031; PMID:3477300
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C;Keywords: duplication; glycoprotein
F;359-66/Domain: transferrin repeat homology <TRH2>
F;222,300,387,485,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2323
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A; Residues: 1-708 < LEP>
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Matches
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Species: Mus musculus (house mouse)

Date: 10-8ep-1999 #sequence_revision 10-8ep-1999 #text_change 10-8ep-1999

Accession: A28438; A41205

Pentecost, B.T.; Teng, C.T.

Biol. Chem. 262, 10134-10139, 1987

Biol. Chem. 262, 10134-10139, 1987

Richtle: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre; Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein STV3070 [imported] - Salmonella enterica subsp. enterica serovar Ty C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connexton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Akture 413, 848-852, 201,
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seron. A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
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hydeoideas 3-707 - PENA-
hydeoideas 3-707 - PENA-
hiu, Y.; Teng, C.T.
Ealol. Chem. 266, 21880-21885, 1991
hydele: Characterization of estrogen-responsive mouse lactoferrin promoter.
hydeles characterization of estrogen-responsive mouse lactoferrin promoter.
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C;Reywords: duplication; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41; DB 2;
Pred. No. 20;
); Mismatches
                                                                                                                                                                                                                      Score 41; DB 2;
Pred. No. 8.3;
1; Mismatches
                                                                                             A;Map position: I
C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
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      A;Experimental source: strain 16M
                                                                                                                                                                                                                      57.7%;
illarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                              90 CFHWKSLRRQVR 101
                                                                                                                                                                                                                                                                                                                                                     1 CFOWKRNMRKVR 12
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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A;Residues: 1-511 <PAR>
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A; Residues: 1-15 <LIU>
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                                    C, Genetics:
A, Gene: BMEI1517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: AG3441

;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

; Mazur, M.; Golteman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess

roc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

Title: The genome sequence of the facultative intracellular pathogen Brucella melitens

Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                le pyridoxamine-phosphate oxidase (BČ 1.4.3.5) [imported] - Brucella melitensis (q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du
Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                            Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium; Reference number: A97359; PMID:11743194
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, cience 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. Reference number: AB2577; PMID:11743193
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Experimental source: strain C58 (Dupont)
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                                                                                                                                                                                                                                                           ross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 2;
Pred. No. 8.2;
1; Mismatches 4
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C,Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                    1,Gene: AGR C 1381
1,Map position: circular chromosome
2,Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.7%;
ilarity 58.3%;
Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                         1-206 <KUR>
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                                                                                                                                         Accession: H97451
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C)Accession: G86506
R)Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Acids Res. 28, 2311-2314, 2000
A)Tattle: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A)Reference number: A86491; MUID:20330349; PMID:10871362
A)Accession: G86506
A)Accession: G86506
A)Accession: Lype: DNA
A)Molecule type: DNA
A)Residues: 1-759 <STO>
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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A;Experimental source: strain J138
C;Genetics: A;Gene: CPj0126
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-447 - VNI2>
A;Residues: 1-477 - VNI2>
A;Cross-references: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN00022; CESP:M18.8
A;Experimental source: clone M18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein M18.8 - Caenorhabditis elegans
C.Species Caenorhabditis elegans
C.Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 29-0ct-1999
C.Accession: T18633; T23799
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Experimental source: clone B0001
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Pred. No. 66;
2; Mismatches
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Molecule type: DNA
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submitted to the EMBL Data Library, January 1996
A;Reference number: Z19800
A;Accession: T23799
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A,Introns: 41/3; 137/1; 326/3; 434/2
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Similarity 66.7%;
6; Conservative
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
Matches 6; Conserv
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QWKKNLRDV 496
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Cispecies: Halobacterium sp. NRC-1
Cispecies: Gor-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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;Species: Chlamydomonas reinhardtii
;Species: Chlamydomonas reinhardtii
;Date: 21-May-1999 #text_change 02-Feb-2001
;Date: 21-May-1999 #text_change 02-Feb-2001
;Mitchell, D.R.; Brown, K.S.
Cell Sci. 107, 635-644, 1994
;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.;Reference number: 216302; MuID:94274778; PMID:8006077
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A; Map position: IX
A; Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/3; 3868/
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A; Cross-references: GB: AE004437; NID: g10581192; PIDN: AAG19967.1; GSPDB: GN00138
C; Genetics:
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Molecule type: DNA
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F;20-707/Product: lactotransferrin #status predicted <MAT> '
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 34;
4; Mismatches 3; Indels
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Pred. No. 2.6e+02;
4; Mismatches 3; Indels
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Best Local Similarity 41.7%;
Matches 5; Conservative
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Matches 5, Conservative
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A;Status: preliminary
A;Molecule type: DNA
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Accession: A48396
(Kruft, V.; Kapp. U.; Wittmann-Liebold, B.)
(Accession: A48396
(Mr. 1991)
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(Mr. 1993)
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(Mr. 1993)
(Accession: A48396
(Mr. 1993)
(Accession: A48396
Status: preliminary
, Molecule type: DNA
, Molecule type: DNA
, Molecule type: DNA
, Molecule type: DNA
, Molecule type: DNA
, Fesidus: 1-759 cARN
, Experimental source: Strain CWL029
, Experimental source: Strain CWL029
, Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Uncleic Acids Res. 28, 1397-1406, 2000
, Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
;Residues: 1-759 <REA>
;Cross-references: GB.AE002222; GB.AE002161; NID:97189553; PIDN:AAF38461.1; PID:9718956
;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bosomal protein 128 - Bacillus stearothermophilus
Species: Bacillus stearothermophilus
Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
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A;Molecule type: protein
A;Residues: 1-60 «Krus
A;Note: sequence extracted from NCBI backbone (NCBIP:69662)
C;Superfamily: Escherichia coli ribosomal protein L28
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Best Local Similarity 66.77
Matches 6; Conservative
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Q99up4 staphylcoco
P29128 ovis aries
Q10353 schizosacch
P43488 mus musculu
P19506 simian immu
Q55185 synechocyst
                              eikenella c
thermoplasm
homo sapien
 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cho Y.Y.;
Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferroxin A;
Lattoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE=Mammary gland;

MEDLINE=90384839; PubMed=2402455;

Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;

"Compler nucleocide sequence of human mammary gland lactoferrin.";

Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB-Nammary gland;
Liang Q., Jimenorz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
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TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                                     TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; O00756; Q9H1Z3; Q96KZ4;
                              P35649 e
P58306 t
Q9ulc6 l
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TISSUE=Mammary gland;
Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]
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submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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088A DROME
SYH CHLMU
MSSI SCHPO
YHAZ EIKCO
PDII HUWAN
RL28 STAAM
                                                                                  RL24_SCHPO
TNF4_MOUSE
VIF_SIVSP
Y495_SYNY3
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TISSUE=Mammary gland;
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IISSUE=Prostate;
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Q9tum0 camelus dro
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caenorhabdi
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                                                                     February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec
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P08071
Q39565
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(c) 1993 - 2003 Compugen Ltd.
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TRFL_CABHI
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DYHBETHEN
NIA_BONSE
NIA_BONSE
NLA_BONSE
NLA_BLIBAF
RL28_LISMO
RPOB_LIBAF
Y125_MYCCA
Y115_MYCCA
Y115_MYCCA
YNR2_CABHI
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CAX1_ARATH
KDG1_ARATH
VP4_ROTGA
PHYC_SORBI
SYB2_RHIME
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CABEL
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Gapop 10.0 , Gapext 0.5
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TISSUE=Mammary gland; MEDLINE=90326549; PubMed=2374734; Powell M.J., Ogden J.E., "Nucleotide Bequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013 (1990).

SEQUENCE OF 3-711 FROM N.A.

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SEQUENCE OF 237-711 FROM N.A.
SEQUENCE OF 237-711 FROM N.A.
MACCOMDIE W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., 1a Bastide M., Kaplan N., Greco T., Touchman J., Marzny D.,
Dragan Y., Giacalone J., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                 "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
Biochim. Biophys. Acta 670:243-254 (1981).
                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedle J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031, PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an expression of manA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                                                           SEQUENCE OF 20-711.
MEDLINE-85076667; PubMed-6510420;
Mera-Bourigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreull J., Jolles P.,
"Human lactorransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'An 88 amino acid long C-terminal sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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MEDLINE=99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                    Eur. J. Biochem. 145:659-666(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 36:341-346(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
B. Gar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
B. Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
"Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998).
I. FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USGNALLY BICARBOWATE.
C. PUNCTION: LACTOFERROXIN A. B. AND C. HAVE OPPIOID ANTAGONIST
ACTIVITY: LACTOFERROXIN A. SONGEMBAT HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS. CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
Tsolation and characterization of opioid antagonist peptides derived from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990). Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998). -i- SUBCELLUTAR LOCATION: Secreted.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY. Acta Crystallogr. D 55:403-407(1999) EMBL; X53961; CAA37914.1; -.
EMBL; U07643; AAB60324.1; -.
EMBL; M93150; AAA36159.1; -.
EMBL; M93202; AAA59511.1; -.
EMBL; M82305; AAA5656.1; -.
EMBL; M18642; AAA86665.1; -. AF332168; AAG48753.1; -. AAH15822.1; -. AAH15823.1; -. THR-30 AND ARG-48. M73700; AAA59479.1; X52941; CAA37116.1; U95626; AAB57795.1; -1- SUBUNIT: MONOMER .-OCT-93 -OCT-93 -- AUG-94 PubMed=9873069; BC015823 LEI; 31 LGB; 31 LFH; 3 BKA; VARIANTS awamori EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; PDB; PDB; PDB; PDB; PDB; 

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Capra hircus (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
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Pred. No. 0.22;
2; Mismatches 2; Indels
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TISSTE-Mammary gland;
TISSTE-Mammary gland;
Lee K., Yu D.; Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRFL CAPHI STANDARD; PRT; 708 AA. Q29477; Q29479; TDEC-1998 (Rel. 37, Casted) 15-DEC-1998 (Rel. 37, Last sequence update) 15-UW-2002 (Rel. 41, Last annotation update) LEGCOLCHARDFERIN PRECURSOR (Lactoferrin) LTF.
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Best Local Similarity 66.7.
8; Conservative
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Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (Uni-199) to the BMBL/Genbank/DDBA databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
-- SANION, USDALLY BICARBONATE (BY SIMILARITY).
-- SUBUNIT: MONOMER (BY SIMILARITY).
-- SUBUNIT: MONOMER (BY SIMILARITY).
-- SUBCELLULAR LOCATION: Secreted.
-- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                       Gaps
                                                                                                                                                                                                                                                                                                                                   Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameluae; Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Somall; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999)
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EMBL; AJ131674; CAB53387.1; -.
HSSP; O77811; 1BLX.
InterPro; 1RR001156; Transferrin.
Pfam; PR00405; transferrin; 2.
PRINTS; PR00421; TRANSFERRIN.
SMART; SM00094; TRER, 2.
PROSTIE; PS00206; TRANSFERRIN.
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                    Length 711;
                Score 67; DB 1; Length 711
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1; Mismatches 0; Indels
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Matches 11; Conservative
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                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iBb-sib.ch).
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                                                                                                                                                                                                                                   EMBL, U53857, AAA97958.1; -.
BRBL, X78902, CAA55517.1; -.
HSSP, O77699, ICE2.
InterPro; IPR001156; Transferrin.
PFINTS, PR00405; transferrin; 2.
PRINTS, PR004094; TRANSFERRIN.
SMART; SM00094; TRANSFERRIN.
PROSTTE; PS00206; TRANSFERRIN.
PROSTTE; PS00206; TRANSFERRIN.
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Pred. No. 0.22;
3; Mismatches 1; Indels
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L -> R (IN REF. 2).
F -> P (IN REF. 2).
F -> P (IN REF. 2).
F -> P (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C8353960D CRC64;
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DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
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1 CFQWKRNMRKV 11 |:||:|||: 38 CYQWQRRMRKL 48

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THE CONTRIL GOORS STRNDARD, PRT; 695 AA.

TOTALL: 1999 (Rel. 38, Creeted)

THE LULL: 1999 (Rel. 38, Creeted)

THE LULL: 1999 (Rel. 38, Last sequence update)

THE LULL: 1999 (Rel. 38, Last sequence)

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                                                                                                                                                                                                                                                  59.2%; Score 42; DB 1; Length 695;
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Bacteria; Firmioutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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Pred. No. 0.69;
2; Mismatches 1; Indels
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SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                  (GLCNAC
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15-JUN-2002 (Rel. 41, Last annotation update)
50S riboscmal protein L28.
RPMB OR TTE1495.
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4; Mismatches
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15-JUN-2002 (Rel. 41, Last seq.
15-JUN-2002 (Rel. 41, Last annomals)
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Best Local Similarity 58.3
Matches 7; Conservative
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695 AA;
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RL28_THETN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991)
J. Biol. TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANTON, USUBALIY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pentecost B.T., Teng C.T., "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                         Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00205; TRANSFERIN 1; 1.
PROSITE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                P08071; P70690, 061799; 0922P2; 01-AUG-1988 (Rel. 08, Created)
15-UNW-2002 (Rel. 41, Last sequence update)
15-UNW-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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LACTOTRANSFERRIN.
1.
                             707 AA.
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J. Biol. Chem. 262:10134-10139(1987).
                         PRT;
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MEDLINE=87280033; PubMed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
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EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
PSSP; P02788; LCB6.
MGD; MGI:96837; Ltf.
InterPro; IPR001156; Transferrin.
STANDARD; Q922P2;
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PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
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EMBL; D88510; BAA13633.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                              COLLED COLL (POTENTIAL).
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
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ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                  EMBL; U02963; AAA19956.1; -.
InterPro; IPR004273; Dynain heavy.
Pfam; PF03028; Dynain heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 4568;
       -!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW; 9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIA_DROME STANDARD; PRT; 292 AA. Q9XZ16; Q9Y391; 20-MXY-2000 (Rel. 39, Created) 30-MXY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Nubula protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB :
Pred. No. 92;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 COILED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 519961
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1778
2017
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33406
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SEQUENCE
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110 IRON 1 (BY SIMILARITY).

210 IRON 1 (BY SIMILARITY).

271 IRON 2 (BY SIMILARITY).

451 IRON 2 (BY SIMILARITY).

451 IRON 2 (BY SIMILARITY).

444 IRON 2 (BY SIMILARITY).

ANION (POTENTIAL).

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J. Cell SCI. 107-1635-644(1994).

J. Cell SCI. 107-1635-644(1994).

-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILLA AND PLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

-!- SUBBUILT: ONSISTER OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            039565;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagilar outer arm.
Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonascaee; Chlamydomonas.
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F26AE0340A4C19A8 CRC64;
2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 4568 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77865 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    707 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
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SEQUENCE FROM N.A.
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                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kruft V., Kapp U., Wittmann-Liebold B.;
"Characterization and primary structure of proteins L28, L33 and L34
"Characterization and primary structure of proteins L28, L33 and L34
Elachimie 73:855-860(L991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                      Science 287:2165-2195(2000).
-!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
-!- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 54.9%; Score 39; DB 1; Length 292; Best Local Similarity 54.5%; Pred. No. 7.9; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dacillus stearothermophilus.
Bacteria, Firmicutes, Bacillales, Geobacillus.
NCBL_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RL28_BACST STANDARD; PRT; 60 AA. P2374; 60 AA. 01-NOV-1991 (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 50S_ribosomal protein L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDLINE-92075758; PubMed=1742360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF147700; AAD33987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0026629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 POWLRSFRRLR 160
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BACST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glaser P., Frangel E., Buckrees C., Rusnick C., Amend A., Baquero F., Barche P., Chartaborty T., Charbit A., Checuani F., Blocker H., Brandt P., Chartaborty T., Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O., Entian K.-D., Febih H., Carcia-del Portillo F., Garrido P., Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurspkat G., Maltunno E., Maltunnam A., Mata Vicente J., Ny E., Nedjari H., Nordaiek G., Novella S., Ge Pablos B., Perez-Diaz J.-C., Purcell R., Varguez-Boland J.-A., Voss H., Wehland J., Cossart P., Cossart P., Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
 -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE 128P FAMILY OF RIBOSOMAL PROTEINS
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                                                                                                                                                              Score 38; DB 1; Length 60;
Pred. No. 2:3;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53.5%; Score 38; DB 1; Length 62; 66.7%; Pred. No. 2.3; Live 2; Mismatches 1; Indels
                                                                                                                           60 AA; 6810 MW; 2AD9161CD60E82F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA43DE039213C562 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                IS-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosemal protein L28.
RPMB OR LMO1816 OR LIN1930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 6991 MW; AA43DE03
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Pfam; PP00830; Ribosomal L28; 1.
TIGREAMS; TIGR00009; L28; 1.
                           FIR, A483-96; A483-96.
InterPro; IPR001383; Ribosomal L28.
Pfam; PF00830; Ribosomal L28; I.
TIGRFAMs; TIGR00009; L28; 1.
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                                                                                                                                                              53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Listeria monocytogenes, and
                                                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1639, 1642;
               PIR; A48396; A48396
InterPro; IPR001383
                                                                                                                                                              Query Match
Best Local Similarity
                                                                                        Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       4 WKRNMRKVR 12
                                                                                                                                                                                                                                                             27 WKANLQKVR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isteria innocua.
                                                                                                                                                                                                                                                                                                                                                               RL28 LISMO
Q92AJZ;
                                                                                                                         SEQUENCE
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RL28_LISMO
                                                                                                                                                                                                     Matches
STX BBBBB
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                                                                                               SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAHLA-BATCC 27343 / KID;
MEDLINE-SO659641; PubMed-4476192;
BOTA M., Gilbert W., Gillevet P.M.;
BOLAM M., Gilbert W., Gillevet P.M.;
"Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology.";
Mol. Microbiol. 16:955-967 (1995).
-1- SIMILARITY: BELONGS TO THE COF/YBHA/XIDA/YIGL (B.COLI) / YCSE/YXEH (B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simian immunodeficiency virus (F236/smH4 isolate) (sooty mangabey). Viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid viruses; Retroid virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus virus
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Man African primate lentivirus (SIVsm) closely related to HIV-2.";
Nature 339:389-392(1989).
-i- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 38; DB 1; Length 267; 58.3%; Pred. No. 11; ive 2; Mismatches 3; Indels
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MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 267
267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 233006; CAA83689.1; -.
InterPro; IPR001454; H1gnase/hydrlase.
InterPro; IPR0010150; Hypothet_cof.
Ffam; PF00702; Hydrolase; I.
PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
Hypothetical protein.
NOM TER 267 267
SEQÜENCE 267 AA; 30425 MW; D5912DD58:
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InterPro; IPR000475; Viral_infect.
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PIR; 807989; 807989.
HIV; X14307; VIF$SMMH4.
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les 7; Conservative
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                    NCBI_TaxID=2095;
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01-OCT-1989
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Planet P., Jagoueix S., Bove J.M., Garnier M.;
"Detection and characterization of the African Citrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Candidatus Liberibacter.
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146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                           RPOB LIBAF STANDARD; PRT; 146 AA. P41187; 01-FBB-1995 (Rel. 31, Created) 10-FBB-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) DNA-directed RNA polymerase beta chain (EC 2.7.7.6) beta chain) (RNA polymerase beta subunit) (Fragment)
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Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
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Pfam; PF00562; RNA pol B; 1.
PROSITE; PS01166; RNA POL BETA; PARTIAL.
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Best Local Similarity
Matches 6; Conserv
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                                                            29 WKANLQKVR 37
4 WKRNMRKVR 12
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SEQUENCE
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Y125 MYCCA
AC P3361,
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Rhabditidae; Peloderinae; Caenorhabditís.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1834 HUMAN STANDARD, PRT, 365 AA.
P30455; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- COFACTOR: FAD (POTENTIAL)
-i- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
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                                                                                                                        Query Match
52.1%; Score 37; DB 1; Length 214;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z35602; CAA84671.2; -.
WormPep; R13G10.2; CE25088.
InterPro; IPR002937; Amino oxidase.
Pfam; PF01593; Amino oxidase. 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD. NP BIND 311 366 PAD (ADP PART) (POTENTIAL).
SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                     214 AA; 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              IS-DEC-1998 (Rel. 37, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
R13G10.2.
Pfam, PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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                                                                                     SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           du Toit E.D., Parham P.;
"Structural diversity in the HLA-AlO family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=99056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93235211; PubMed-8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
HLA-A OR HLAA.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with serology.";
Tissue Antigens 41:72-80(1993)
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal; Polymorphism.
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/FTIC=VAR 004379.

K -> N (IN A*3402).

/FTIC=VAR 004380.

R -> I (IN A*3402).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interallelic conversion.";
J. Immunol. 149:3411-3415(1992).
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EMBL; X61705; CAA43873.1; -...
PIR; S16771; S1677.
HSSP; O19673; 11458.
MIM; 142800; -...
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
Pfam; PF00129; MHC_I; 1...
Pfam; PF00129; MHC_I; 1...
ProDom; PD000050; MHC_I; 1...
SMART; SM00407; IgGl; 1...
PROSITE; PS00290; IG_MHC; 1...
RAGINAL Transmembrane; Glycoprot SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmembrane SIGNAL Transmemb
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							5 CRC64;
129 129 P -> S (IN A*3402). /FTId=VAR 004382.	Q -> R (IN A*3402)	/FTId=VAR 004383.	W -> L (IN A*3402)	/FTId=VAR 004384.	L -> I (IN A*3402)	/FTId=VAR 004385.	OG3BFG3EGEGEO1F
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129	138		180		312		41055
							AA;
129	138		180		312 3		365
VARIANT	VARIANT		VARIANT		VARIANT		SEQUENCE
F.F.	F.	I.H	FŢ	Ц	FI	HH	Š

4 WKRNMRKVR 12 | | | | | | | | 84 WDRNTRKVK 92 ò

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0; Gaps

Query Match
50.7%; Score 36; DB 1; Length 365;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 2; Indels

Search completed: February 21, 2003, 07:51:38 Job time : 6.2093 secs

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017549 caenorhabdi

091jiz5 mus musculu

092955 chlamydia p

062582 chlamydia p

062582 chlamydia p

088745 encephalito

090884 human immun

097855 human immun

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08871 cicer ariet

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081437 arabidopsis

099165 arabidopsis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OLIMAY-2000 (TREMBLrel. 13, Created)
01-MAY-2000 (TREMBLrel. 13, Last sequence update)
01-JUN-2001 (TREMBLrel. 17, Last annotation update)
10-JUN-2001 (TREMBLRel. 17, Last annotation update)
Hactoferarin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Straubberg R.; Straubberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 AA.
                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                       Q9SML2
Q68541
Q8YP77
Q8TAX2
Q9F7Y4
                          O62582
Q8SRG3
Q8SQI6
O90884
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Q9QU30
Q9W1D5
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          Q9JJZ5
Q9Z955
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O81653
Q9ZTP0
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Q92RH8
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Q8S487
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
  Query Match
Best Local Similarity 90.9
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
 Lactotransferrin.
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 Q8TCD2
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1D 09UC)
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OB. HOMO
OC EUKRA
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Q8TCD2
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Q9uvy5 homo sapien
Q9tr90 coust aries
Q93780 caenorhabdi
Q8r9u1 thermoanaer
Q986a thizobium 1
Q8th8 thizobium m
Q87th8 thizobium m
Q87th8 thizobium m
Q87th8 thizobium m
Q97th3 thomo sapien
Q97th1 homo sapien
Q97th3 thizobium ind
Q97th3 thizobictri
Q97th3 thizobictri
Q90m21 homo sapien
Q97th3 thizobictri
Q80m21 homo sapien
Q97th3 thizobium 1
Q87th2 thizobium 1
                                                                      (without alignments)
114.078 Million cell updates/sec
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                                                            February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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                                                                                                                                                                                  671580
        GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                              Potal number of hits satisfying chosen parameters:
                                                                                                                                                                671580 seqs, 206047115 residues
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                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
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Q9UCY5
Q9UCY5
Q83780
Q83780
Q8CA0
Q8UHC2
Q9ZRH8
Q9ZRH8
Q9ZRH8
Q9ZRH8
Q9ZRH9
Q9QHPA3
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sp_bhage:*
sp_lant:*
sp_virus:*
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sp_unclassified:*
sp_unclassified:*
sp_runclassified:*
                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                            sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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4aximum DB seq length: 200000000
                                                                                              US-09-743-107B-91
                                                                                                                  1 CFQWKRNMRKVR 12
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Perfect score:
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PRT;
  SEQUENCE FROM N.A.
MEDLINE=99069613; Pubmed=9851916;
                                                                                                                                                                                                                                                                                                                                                           Thermoanaerobacter tengcongensis.
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                                                                                                                    / Match 63.4%; Local Similarity 72.7%; nes 8; Conservative
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Matches 7; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                                                                                                                                                                                                                                                                                Ribosomal protein L28. RPMB OR TTE1495.
                                                                                                                                                                                        262 FQWKISMRKTR 272
                                                                                                                                                                         2 FOWKRINMRKVR 12
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SEOUENCE 62 AA;
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Matches
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                          "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae; Caprinae; Ovis.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                ch 81.7%; Score 58; DB 4; Length 38; 1 Similarity 90.9%; Pred. No. 0.0019; 10; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 6; Length 33;
Pred. No. 0.16;
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=95127729; PubMed=7827104;
MEDLINE=95127729; PubMed=7827104;
MIGHAN Z.Y., Jolles P., Migliore-Samour D., Flat A.M.;
Blochim. Blophys. Acta 1243:25-32 (1995).
HSSP; O77698; JCE2.
HSSP; O77698; JCE2.
HSSP; O77698; LCE2.
FEAM; PF00405; transferrin.
FEAM; PF00405; transferrin; I.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                          Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNJ-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fregment).
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Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
                                                                                      seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                  MEDLINE=96081613; PubMed=8551695;
                                                                                                                            InterPro, IPR001156; Transferrin.
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54.5%;
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F53H4.4.
Caenorhabditis elegans.
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Matches 10; Conser
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Matches 6; Conser
                                     SEQUENCE FROM N.A.
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             NCBI_TaxID=9606;
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Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBL_TaxID=119072;
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EMBL; AE013107; AAM24713.1; --
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Rhizobium loti (Mesorhizobium loti).
Shizobium loti (Mesorhizobium loti).
Bacterial Froteobacteria, alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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SEQUENCE FROM N.A.
MEDLINE=21082930; PubMed=11214968;
Maneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamotc
Kaneko T., Nakamura Y., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Katanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y.; Kiyokawa C., Kohara M., Matsumoto M.,
"Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 16; Length 62;
Pred. No. 3.6;
2; Mismatches 1; Indels
                                                                                                                                                                                                Score 45; DB 5; Length 275;
Pred. No. 3.1;
                                investigating biology.";
Science 282:2012-2018(1198).
EMBL; 281089; CAB03137.1; ..
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTN-2002 (TEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
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1 CFOWKRNMRKVR 12
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                       Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-2166856); PubMed-11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okutau V.K., Zhou Y., Chen L., Wood G.E., Almaida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Cardenord, Kaupavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Cardon C., Rowen G., Samphimmachak C., Wu Z., Romero P., Gordon D., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.; Ingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.

MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Gurollo B., Goldman B.S., Cao Y. Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TYEMBLrel. 21, Created)
01-JUN-2002 (TYEMBLrel. 21, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
Pyridoxamine 5. phosphate oxidase.
PDXH OR ATU0760 OR AGR C 1381.
Agrobacterium tumefaciene (strain C58 / ATCC 33970).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                               57.7%; Score 41; DB 16; Length 205; 58.3%; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                            205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                               Mescrhizoblum loti.";
DNA Res. 7:331-338(200).
EMBL; AP003011; BAB5353.1; -.
InterPro; IPR00659; Pyridox_oxidase.
Fram, PP01243; Pyridox_oxidase, 1.
ProDom; PD006312; Pyridox_oxidase; 1.
TIGRFAMs; TIGR00558; pdxH; 1.
Complete PROSITE; RS01064; PYRIDOX_OXIDASE; 1.
SEQUENCE 205 AA; 23300 WW; OBADE4CD3
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                                                                                                                                                                                                                                                                                                                                                  Query Match
Query Match
Best Local Similarity 58.33,
Best Local Similarity 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFOWKRNMRKVR 12
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE 206 AA;
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A Bolstard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
Bolstard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Rahn D., Kise E., Lelaure V., Masuy D.,
Pohl T., Portetelle D., Rannelle B., Ramaperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
Sinorhizoblum mellioti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
R EMBL; AL591785; CAC4547.1;
R EMBL; AL591785; CAC4547.1;
R FREE, PROLS43; Pyridox oxidase.
R Probom, PD006312; Pyridox oxidase.
R Probom, PD006312; Pyridox oxidase.
R TICRRAMS; TICRR0588; pox4;
R PROSITE; PS01064; PYRIDOX_OXIDASE; UNICHOWN_1.
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STRAIN=16M / ATCC 23456 / BIOTYPE 1;

STRAIN=20020109; PubMed=11756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

"The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DTA-2002 (TrEMBLrel. 21, Last senotation update)
01-DTA-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein (EC 1.4.3.5).
PDXH OR R00895 OR SWC00069.
Rhizobium mellioti (Sinorhizobium mellioti).
Rhizobiaceae; Sinorhizobium: alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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Brucellaceae; Brucella.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase, Complete Proteome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
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58.3%; Pred. No. 12;
cive 1; Mismatches 4;
                                                                                                                                                        206 AA.
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                                                                                                                                                        PRELIMINARY;
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Best Local Similarity 58.3
Matches 7; Conservative
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88 CFHWKSLRRQVR 99
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Local Similarity 66.7
nes 6; Conservative
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les 6; Conservative
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         SEQUENCE FROM N.A.
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69 EWKENLRKV 77
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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Pred. No. 31;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                    Query Match 57.7%; Score 41; DB 16; Length 208; Best Local Similarity .58.3%; Pred. No. 12; Matches 7; Conservative 1; Mismatches 4; Indels
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL, AE009587; AALSZ698.1; -
InterPro; IPRO00559; Pyridox_oxidase.
Ffam; PF01243; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
ProDom; PTGRFM'8; TIGR00558; pdxH; 1.
PROSTIE; PS01064; PYRIDOX_OXIDASE; 1.
Oxidoreductase; Complete Proteome.
SEQUENCE 208 AA; 23866 MM; CB1F50BC9612DE28 CRC64;
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EMBL, AL672756; CAD06049.1; -
HYpothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 WW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Glycoprotein gpl20 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Matches 7; Conservative
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SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=2004970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
STRAIN=NJS182;
Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,
Apeagyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N.,
Ishikawa K., Sata T., Kurata T.;
"Genetic and phylogenetic analysis of HIV-1 strains from Southern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
NCBI_TaxID=4182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%; Score 40; DB 15; Length 81; 66.7%; Pred. No. 7.1; tive 2; Mismatches 1; Indels
                                                                                                                                                      Ghana.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ225659; CAA12841.1;
Interpro; IFPO077; GP120.
Pfam; PF00515; GP120; 1.
AIDS; Coat protein; dlycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                81 AA; 9138 MW; 2D43DCD554295572 CRC64;
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01-NVV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FL32891 fis, clone TESTI2004929
Homo sapiens (Human).
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J. Agric. Food Chem. 47:4932-4938 (1999).

EMBL, PROSS 11, AAD-243.1; -.

Interpro; IPROSS 12, AAI.

Interpro; IPROSS 17, AAI.

Interpro; IPROSS 17, AAI.

Interpro; IPROSS 17, AAI.

FEAM; PROS34; tryp_alpha_amyl; 1.

PRINTS; PROS34; tryp_alpha_amyl; 1.

SMART; SMARY; 1.

SEQUENCE 148 AA; 17524 MW; BA46B033BA
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Search completed: February 21, 2003, 08:00:44 Job time : 21.6744 secs
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MEDLINE=20504483; PubMed=11016950;

MEDLINE=20504483; PubMed=11016950;

A Gukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Frebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lower T.M., Liang P., Riley M., Hood L., DasSarma S.;

"Genome sequence of Halobacterium species NRC-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                   TISSUE=TESTIS;
Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Isono Y., Kawai-Hio Y., Sato H., Mshikawa T., Kimura K., Yamashita H., Marasuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugiyama A., Kawakami B., Suzuki Y., Sugino S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Masuho Unu acquencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOS7453; BAB71493.1;
SEQUENCE 274 AA; 30083 MW; IDD43654D4135B2F CRC64;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 56.3%; Score 40; DB 4; Length 274; Best Local Similarity 50.0%; Pred. No. 25; Matches 6; Conservative 3; Mismatches 3; Indels
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Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriacae; Halobacterium.
NCBI_TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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4; Mismatches
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InterPro, IPR001622, K+channel pore.
Pfam, PF00805, Pentapeptide, 2
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01-WAR-2001 (TrEMBLrel. 16,
01-MAR-2002 (TrEMBLrel. 20,
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blosyntheeis genes in Rhizobium leguminosarum bv. viciae VF39.";
Mol. Biol. (Mosk) 32:797-804 (1998).
EMBL, AF028810, AAB8891.1;
Hypothetical protein.
SEQUENCE 273 AA; 30986 MW; F195D2FBF7AD44D3 CRC64;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein
Hypothetical lano a protein
Khizoblum leguminosarum (biovar viciae).
Bacteria, Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizoblaceae; Rhizoblum.
                                                                                                                                                                                                                                                                                                                                                                           Structural and functional organization of the exopolysaccharide
                                                                                                                                                                                                                                                                                                      MEDLINE=99113394; PubMed=9914965;
Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.,
Ksenzenko V.N.;
                                                                                                                                                                                            STRAIN=VF39;
Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Matches 6; Conserv
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RESULT 1
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                                                                                                                                     February 21, 2003, 07:37:21; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SIDE2/gcgdata/geneseq, geneseqp_embl/AA1990.DAT:
| SIDE2/gcgdata/geneseq_geneseqp_embl/AA1990.DAT:
| SIDE2/gcgdata/geneseq_geneseqp_embl/AA1991.DAT:
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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## ALIGNMENTS

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                             Dolphin GT;
                                                                        Human lactoferrin derived peptide SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                             Baltzer L,
           AAY78091 standard; Peptide; 12 AA
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17-JUL-1998; 98SE-0002562.
29-DEC-1998; 98SE-0004614.
                                                     (first entry)
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                                                                                                                                                                                WO200001730-A1.
                                                                                                                                                 Homo sapiens.
Synthetic.
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                                                     25-APR-2000
                                                                                                                                                                                                     13-JAN-2000.
                                AAY78091;
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WPI; 2000-147388/13.

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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:92.
                           Claim 22; Page 38; 102pp; English.
                                                                                                                                                                                                                                          AAY78092 standard, Peptide, 12 AA
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98SE-0002562.
98SE-0004614.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as usinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bacterioidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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98SE-0004614.
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                                                                                                                                        AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. Cungicidal and bactural and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot the used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.1e-05; ive 0; Mismatches 0; Indels
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12 AA;

Sequence

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. C fungicidal and bactericidal and may also be used as preservatives. C by though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservativa
                                                                                                                                                                                                                        Gaps
fungicidal and bactericidal and may also be used as preservatives
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                                                                                                                                                                               Score 67; DB 21; Length 12;
Pred. No. 9.7e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     AAY78046 standard; Peptide; 12
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                            1 CFQWQRNMRKVR 12
                                                                                                                                                                                                                                                         CFOWKRINMRKVR 12
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                                                                                                                                               12 AA;
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                  Human, lactoferrin, modification, infection, inflammation, tumour;
food, infant formula, anti-inflammatory, anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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          DB 21; Length 12;
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Pred. No. 9.7e-05;
1; Mismatches 0; Indels
Score 67; DB 21; December of No. 9.7e-05; Pred. No. 9.7e-05;
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                                         1; Mismatches
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                                                                                                                                                                                    AAY78047 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
        94.48;
91.78;
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Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                      (first entry)
                                         11; Conservative
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                                                                        1 CFQWKRNMRKVR 12
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      Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                         1 CFQWQRNMRKVR
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AAY78037 standard; Peptide; 13 AA.

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AAY78001 to AAY78100 represent peptides having sequence based on human latcoferrin. The peptides are taken up in the intestine through actoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urihary tract infections, collits, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fundicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                             Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial, anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:37.
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98SE-0002562.
98SE-0004614.
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                                                                                    (first entry)
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Best Local Similarity 91.7-
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                               Homo sapiens.
Synthetic.
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                                         AAY78037;
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ID AAY7
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                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Page 36; 102pp; English.
                                                                                                                                             AAY78084 standard; Peptide; 12 AA
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98SE-0002562.
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Best Local Similarity 91.7
Matches 11; Conservative
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                      1 CFCWORNMRKVR 12
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17-JUL-1998;
29-DEC-1998;
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Human lactoferrin derived peptide SEQ ID NO:48.

RESULT 7

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Length 13; Indels

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Synthetic.
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        Human, lactoferrin; modification; infection; inflammation; tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative
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Pred. No. 0.00011;
1; Mismatches 0; Indels
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91./v,
Best Local 11; Conservative
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                                                                                                                                                                                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 AA;
                                                                                                                                           40200001730-A1.
                                                                                         Homo sapiens
                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                             06-JUL-1998;
17-JUL-1998;
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                                                                                                                                                                            13-JAN-2000
                                                                                                            Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection (such as membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicial and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, lactoferrin, modification, infection; inflammation; tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.4%; Score 67; DB 21; Length 13; 91.7%; Pred. No. 0.00011; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                        Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78036 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                      Hanson LA, Mattsby-Baltzer I,
                                                                                                                               98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                      99WO-SE01230
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                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 AA;
WO200001730-A1
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                                                                                                                               06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                      36-JUL-1999;
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                                           13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000
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Hanson LA,

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67; DB 21; Length 14;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:51
  Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                  Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY78051 standard; Peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.4%;
ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-SE01230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bactericidal, preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-APR-2000 (first entry)
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Best Local Similarity
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                                          WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 AA;
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29-DEC-1998;
Hanson LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                             AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food sulfs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%; Score 67; DB 21; Length 14; 91.7%; Pred. No. 0.00011; ive 1; Mismatches 0; Indels
                                                                                                                                                Baltzer L, Dolphin GT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                              Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78050 standard; Peptide; 14 AA.
                                                                                                                                              Mattsby-Baltzer I,
                  98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                                                  WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 AA;
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               06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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Synthetic.
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Sequence

Query Match

Matches

ð 셤 AAY78050;

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Gaps . 0

0; Indels

Dolphin GT;

AAY78035 standard, Peptide, 15 AA.

Claim 18; Page 75; 102pp; English.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food suuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR98531-54 are peptides used in an anti-ulcer agent. The agin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                              Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 94.4%; Score 67; DB 17; Length 15; Local Similarity 91.7%; Pred. No. 0.00012; les 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - has low toxicity, is
                                                                                                                                                                                                                                                                                                                                            Score 67; DB 21;
Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-ulcer agent contg. peptide -
heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 11; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                            94.48;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide for anti-ulcer agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-0283869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                1 CPOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFQWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-318857/32
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            14 AA;
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                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                               Matches
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ID AAR9
%X00000000000000X8
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as unimary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

The perfect of the peptides and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                      food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                           modification; infection; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.4%; Score 67; DB 21; Length 15; 91.7%; Pred, No. 0.00012; rive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dolphin GT,
                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 69; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                           Human; lactoferrin;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1998;
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29-DEC-1998;
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AC AAY780
AAY78035

AAY78035

AAY78035

AAY7

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Gaps

Best Loca Matches

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or through the circulation. A medicinal product of the peptide or fragment or thrary tract infections. Collis, and Candida infections (such as urinary tract inflammations and/or tumours. The peptides can also be used for the peptides are also fundicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used allocation and acti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                    Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
uvrinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                    Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 81; 102pp; English
                  25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                    06-JUL-1999;
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98SE-0002441. 98SE-0002562. 98SE-0004614.

Dolphin GT;

Query Match 94.4%; Score 67; DB 21; Length 15; Best Local Similarity 91.7%; Pred. No. 0.00012; Matches 11; Conservative 1; Mismatches 0; Indels 15 AA;

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0; Gaps

1 CFOWKRNMRKVR 12 CFOWORNMRKVR 15 Search completed: February 21, 2003, 07:56:44 Job time : 28.093 secs

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Sequence 3, Application US/08204487

Sequence 3, Application US/08204487

GENERAL NO. 5565425

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, NACKI

APPLICANT: MARASHIMA, HIDEKI

APPLICANT: MARASHIMA, HIDEKI

APPLICANT: DOSAKO, SHIMY I CHI

APPLICANT: TAWASAKI, YOSHIMIRO

APPLICANT: KAWASAKI, YOSHIMIRO

APPLICANT: WANASAKI, YOSHIMKI

TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION

TITLE OF INVENTION: INHIBITORS

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: PATERT ADMINISTRATOP """

STREFT:

ATREFT:

ATREFT:

ATREFT:

ADDRESSEE: THIBEAIT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFCATION: 514
ATTORNEY/AGENT INFORMATION:
ARGISTATION NUMBER: 32.563
REFERENCE/ODCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE: CHRAACTERISTICS:
LENGTH: 18 amino acids
TOTAL COMPANION ACIDS
TELENGTH: 18 amino acids
TELENGTH: 18 amino acids
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CITY: BOSTON
STATE MA
US-08-464-182A-2
US-08-424-1632-2
US-08-421-632-2
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RY: USA
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    February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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/cgn2_6/ptodata1/liaa/5A_COMB.pep:*
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/cgn2_6/ptodata1/liaa/backfiles1.pep:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-68-98-8

US-08-68-98-8

US-07-95-161h-3

US-07-911-174-3

US-07-911-174-3

US-08-204-487-1

US-08-216-71-25

US-08-26-71-25

US-08-26-71-25

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-09-508-74-4

US-09-508-74-4

US-09-508-74-4

US-09-508-74-8

US-07-81-174-8

US-07-81-174-8

US-07-81-174-8

US-07-81-174-8

US-07-81-174-8

US-08-26-71-30

US-08-26-71-30

US-08-31-984-29

US-08-31-984-29

US-08-26-71-30

US-08-31-984-29

US-08-31-984-29

US-08-31-984-29

US-08-464-182h-6

US-08-464-182h-6

US-08-66-271-6

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US-08-66-271-6
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                                                                                                                                                                                                                                                                             262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 20000000000
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Match Length
                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                     Minimum DB seq
Maximum DB seq
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                                                                                                       Run on:
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GENERAL INFORMATION:

APPLICANT: LI, YONG MING
APPLICANT: UL, YONG MING
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF INVENTION: AGE-MEDIATED
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
CONTEX: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-055-8

Sequence 8, Application US/08475055

Sequence 8, Application US/08475055

GENERAL INFORMATION:
APPLICANT: YOM MING LI
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: AND PRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
COMPOTER: ISM PC compatible
COMPOTER: ISM PC compatible
COMPOTER: ABTENTIN Release #1.0, Version #1.25
SUGNERS: APPLICATION NUMBER: US/08/628,380
FILING DATE: APRIL 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Eq. David A.
REGISTRATION NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: 201 343-1684
TELEFRAX: CHARACTERISTICS:
LENGTH: A main a acids
LENGTH: A main a acids
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Pred. No. 9.9e-05;
                                                                                                   Sequence 8, Application US/08628380 Patent No. 5891341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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Best Local Similarity 91.7
Matches 11, Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NOW MING LI
APPLICANT: WORD MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHON AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
CONTRY: USA
                                                                                                                                  0; Gaps
                                                                                 Query Match 94.4%; Score 67; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 9.9e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
FILING DATE: UNB 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION: 436
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
TELEPHONE: SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
94.4%; Score 67; DB 2;
Best Local Similarity 91.7%; Pred. No. 9.9e-05
Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                            US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 internal
                                                                                                                                                                                 1 CFOWKRNMRKVR 12
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US-08-485-948-8
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Gaps

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CLONE:
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                                                                                              US/07/755,161A
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                 SOFTWARE: Displaywite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755
FILING DATE: 19910905
CLASSIFICATION: 530
FICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALKEN INFORMATION:
NAME: WALKEN INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.48;
               OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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AUTHORS:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL ITYPE:
CELL ITYPE:
CELL LINE:
CRAMBILE:
IMMEDIATE SOURCE:
LIBMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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FRAGMENT TYPE;
ORIGINAL SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1:
MOLECULE TYPE:
HYPOTHETICAL:
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JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE; Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STREET: B.C.
COUWIRY: U.S.A.
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
                                                                                                                                      CLASSIFICATION DATA:

CLASSIFICATION DATA:

APPLICATION NUMBER: 08/485,948

FILING DATE:

APPLICATION NUMBER: 08/488,217

FILING DATE: JUNE 7, 1995

APPLICATION NUMBER: 08/418,642

FILING DATE: APRIL 7, 1995

ATORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 947-1-008A

TELEPHONE: 201 343-164

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

WARDER AND ACIDS

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
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94.4%; Score 67; I
Best Local Similarity 91.7%; Pred. No. 9.
Matches 11; Conservative 1; Mismatche
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
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US-07-755-161A-3
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NAME/KEY: modified site

LOCATION: 19

LOCATION: 19

LOCATION: 19

LOCATION: 19

LOCATION: 19

LOCATION: 19

LOCATION: 10

OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond wit)

PUBLICATION: thiol group of Cys residue at location 2"

AUTHORS:
                                                      _____note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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APPLICANT: NAKABILON
APPLICANT: NAKASHINA, HIDEKI
APPLICANT: NAKASHINA, HIDEKI
APPLICANT: NOSUCHI, WATRAU
APPLICANT: NOSUCHI, WATRAU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: NAWASKI, YOSHIHIRO
APPLICANT: HILBITORS
NUMBER OF SEQUENCES: SI
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, Version #1.25
COMPUTER: IBM PC compatible
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COMPUTER: IBM PC COMPATION:
APPLICATION NUMBER: 32,503
REFIRENCE/DOCKET NUMBER: FUN-019
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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Pred. No. 0.00011;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE:

DOCUMENT NUMBER:

FILING DATE:

FULING DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%;
91.7%;
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: Cys
OTHER INFORMATION: thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
ISSUE:
PAGES:
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                                            Gaps
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0
                                        Indels
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Patent No. 5317084

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

ITLE OF INVENTION: Antimicrobial Peptides and an ITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STRRET: 805 Fifteenth Street, N.W., #700
      Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WESTINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY 1992
CLASSIFICATION NUMBER: US/07/891,174
FILING DATE: 05-MAY 1992
ATTORNEY/AGENT IRFORMATION:
APPLICATION NUMBER: US 07/755,161
ATTORNEY/AGENT IRFORMATION:
NAME: WATTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
RELEPRANCE/DOCKET NUMBER:
TELEFRANCE/DOCKET NUMBER:
TELEFRANCE/CONTERMATION:
TELEFRANCE/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
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DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                      1 CFOWKRNMRKVR 12
                                                                                                                                        2 CFOWQRNMRKVR 13
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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US-07-891-174-3
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Gaps
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| Patent No. 5656591
| GENERAL INFORMATION:
| APPLICANT: Mamoru TOMITA et al.
| TITLE OF INVENTION: PRODUCTS THEREWITH
| TITLE OF INVENTION: PRODUCTS THEREWITH
| NUMBER OF SEQUENCES.
| ADDRESSES: Wenderoth, Lind & Ponack
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| OTHER INFORMATION: /note= "Cys residues are protected to
| OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
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                                                              Score 67; DB 1; 1
Pred. No. 0.00011;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 1; ]
Pred. No. 0.00011;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500 kb
COMPUTER: Diskette, S.25 inch, 500 kb
COMPUTER: Mordportect 5.1
CURBNY APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIPICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
NAME: WATEN N. Check, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                    1 CFQWKRNMRKVR 12
                                                                                                                                                                                                                                                      2 CPOWORNWRKVR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                           Query Match
Best Local Similarity
Matches 11; Conserv
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STRANDEDNESS: si
   US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-256-771-25
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US-08-381-984-24
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Patent No. 565691

GENERAL INFORMATION:
APPLICANT: Mannoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
ITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES. 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
GITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 1; Length 20;
Pred. No. 0.00011;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                            /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDULUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IDM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
CLASSIFICATION 1974
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
F
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.48;
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INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                  LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                              ) LOCATION: 1.20
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-204-487-1
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                                                                                                                                                                                                                                                                                NAME/KEY: Peptide
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FALLET NO. 04.2309
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL SAMPAIGN MASS PRODUCTION method of lactoferrin polypeptide from yeast an TITLE OF INVENTION: useful microorganism thereof FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION WUMBER: US/09/508,734
CURRENT FILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-13
NUMBER: OF SEQ ID NOS: 12
SOFTWARE: KOPALCHIN 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
| LOCATION:
| IDBNITECATION NETHOD:
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage US-08-381-984-25
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Pred. No. 0.00011;
1; Mismatches 0; Indels
                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
TLING DATE: THORWATION:
NAME: WATEN M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEFONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09508734 Patent No. 6423509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX:
INFORMATION: OR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 20 antho acids
TYPE: amino acid
STRANDEDNES: single
TOPOLLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.77
Watches 11; Conservative
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                                                                            STREET: 805 ...
                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-508-734-4
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DENTIFICATION METHOD:
COTHER INFORMATION: /note= "the specified peptide as well as
COTHER INFORMATION: peptides including the specified peptide as a fragment thered
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 5.1
COMPUTER: Mordperfact 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION 2752
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL TONE SEQUENCES:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: ADDRESSE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERSONG/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-08-381-984-25
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CLOUR:
CHROMOSOME/SEGMENT:
MAP POSITION:
WAP POSITION:
WAP POSITION:
UNITS:
CHROMOSOME/SEGMENT:
WAP POSITION:
UNITS:
CHROMOSOME/SEGMENT:
WAP CATULOR:
UNITS:
COTHER INFORMATION:
COTHER IN
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 antho acids
TYPE: ANINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWKRNMRKVR 12
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
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VOLUME:
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US-09-508-734-6
US-09-508-734-6
Sequence 6 422509
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                                                                                                                                                                                       Score 67; DB 4; Length 22;
Pred. No. 0.00012;
1; Mismatches 0; Indels
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US-07-755-161A-10
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
PAPENT NO. 5304633
FORTHING NATION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPENDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Weahington
STATE: D.C.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION WNSER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                   Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                             TYPE: PRT CRGANISM: Homo sapiens US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                  1 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                            2 CFQWQRNMRKVR 13
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Matches 11, Conserva
LENGIH: 22
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond wit)
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 94.4%; Score 67; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 0.00013; Matches 11; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                            FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                          TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
DATE:
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RESULT 15
US-07-891-174-10
Sequence 10, Application US/07891174
Sequence 10, Application US/07891174
Sequence 10, Application US/07891174
Sequence 10, S137084
FEREAL INFORMATION:
TILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES:
ADDRESSES: Wenderoth, Lind & Ponack
STRETT: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500Xb
COMPUTER: BEN Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayMrite
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayMrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 20-MAY-1992
CLASSIFICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
TELEFAX: 202-371-8856
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGHT: 25 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TYPE: AMINOTHERICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: modified site.
LOCATION: 21
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LOCATION: 4
IDENTIFICATION METHOD:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL ITYRE:
CRIL INVE:
ORGANELLE:
INMEDIATE SOURCE:
LIBBARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl

Sequence 30, Sequence 32, Sequence 28,

Sequence 2, 7 Sequence 16, Sequence 11,

Sequence 119, Sequence 119, Sequence 119, Sequence 14, A Sequence 6, A Sequence 24,

Sequence 194, App Sequence 4, Appli Sequence 12129, Sequence 13026,

ALIGNMENTS

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94.4%; Score 67; DB 9; Length 15; 91.7%; Pred. No. 5.1e-05; ive 1; Mismatches 0; Indels
0 US-09-978-697-119
0 US-09-978-192A-119
0 US-09-978-182A-119
0 US-09-978-182A-119
0 US-09-978-182A-119
0 US-09-981-649A-24
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0 US-09-981-649A-32
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0 US-09-893-625B-18
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0 US-10-12-904-38
0 US-10-176-918-38
0 US-09-815-242-1313026
0 US-09-815-242-1313026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Georgence 2, Application US/09798869
Publication No. USZ0030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKNAL
APPLICANT: LARS VORLAND
ITILE BOT INVENTION: BIOACTIVE PEPTIDES
ITILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PT/GB99/02851
PRIOR APPLICATION NUMBER: PT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ for Windows Version 4.0
SERIOTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION: APPLICANT: OTHN SIGURD SVENDSEN; APPLICANT: (YSTEIN REKRAL); APPLICANT: BALDUR SVEINBJ (RNSSON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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CORGANISM: HOMO SAPIENS
US-09-798-869-2
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                                   RESULT 2
US-09-798-869-20
        Sequence 6, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 29, Appli
Sequence 4705, Appli
Sequence 4705, Appli
Sequence 4705, Appli
Sequence 41002, A
Sequence 41002, A
Sequence 41002, A
Sequence 5715, Appli
Sequence 61002, A
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Sequence 119, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                       February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54:162 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/PUS NEW PUB.pep:*

2: /cgn2_6/ptodata/3/pubpaa/PUS NEW PUB.pep:*

3: /cgn2_6/ptodata/3/pubpaa/PUS06_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBGOMB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US07_PUBGOMB.pep:*

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14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
                    GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-09-738-626-5715
US-09-925-301-1248
US-09-978-295A-119
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US-09-888-320-2
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US-00-023-066-2
US-00-023-066-2
US-09-798-869-6
US-09-798-869-3
US-09-798-869-3
US-09-798-869-7
US-09-798-869-7
US-09-798-869-2
US-09-798-869-8
US-09-798-869-8
US-09-798-869-8
US-09-798-869-8
US-09-798-869-8
                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                              156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                               US-09-743-107B-92
                                                                                                                                                                                                    1 CFQWKRNMRKVR 12
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Match 1
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Perfect score:
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                                                                                                                                                                                                     Sequence:
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No.
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-6
Query Match 94.4%; Score 67; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.0017; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 59; DB 9; Length 15;
Pred. No. 0.001;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 50; DB 9;
Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURREAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: GYSTEIN REXOLA.
TITLE REPERENCE: BIOACTIVE PEPTIDES
TITLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-31
SOFTWARE PERSECT ON WIMBER: GB9818938.4
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARTSEQ FOR WINGOWS VERSION 4.0
SSOFTWARE: PARTSEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                        Sequence 6, Application US/09798869 Publication No. US20030022821A1
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                   22 CFQWQRNMRKVR 33
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                                                                           1 CFOWKRNMRKVR 12
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Best Local Similarity
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                                                                                                                                                                                      US-09-798-869-6
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APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                     Score 67; DB 9; I
Pred. No. 8.2e-05;
1; Mismatches 0;
   10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAX-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFENCE/DOCKET NUMBER: 31,409
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10023096
Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     ch
l Similarity 91.7%;
11; Conservative
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amino acid
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                                                                                                                                                                                                                                                              ) ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWKRINMRKVR 12
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFQWQRNMRKVR 14
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Matches
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Score 41; DB 9; Length 25;
Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                  APPLICANT: (YSTEIN REGOLA
APPLICANT: (YSTEIN REGOLA
APPLICANT: BALDUR SYZINBJ (RNSSON
APPLICANT: LARS VORLAND
TILLE OF INVENTION: BLOACTIVE PERTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION UNDRER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
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APPLICANT:
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APPLICANT:
GYSTEIN BIOACTIVE PEPTIDES
FILE REFERENCE:
APAGOS OURAND:
GURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
FRIOR APPLICATION NUMBER:
GROUP GROUP
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                                                                                                                                                                                                                           Sequence 4, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.7%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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; ORGANISM: MURINE
US-09-798-869-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-4
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OTHER INFORMATION: synthetic peptide (modified form of homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.2%; Score 42; DB 9; Length 15; Best Local Similarity 54.5%; Pred. No. 0.55; Matches 6; Conservative 3; Mismatches 2; Indels
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   1; Indels
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APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEO THARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 15
   3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/799,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                       US-09-798-869-23
Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED
APPLICANT: GYSTEIN REKDAL
APPLICANT: BALDUK SVEINEJ (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09798869 Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 63.6
Matches 7; Conservative
7; Conservative
                                                                                                        3 CYQWQRRMRKL 13
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                                                                  1 CFOWKRNMRKV 11
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ORGANISM: CAPRINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-23
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LENGTH: 25
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   Matches
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RESULT 11
US-09-798-689-8
; Sequence 8, Application US/09798869
; Publication No. US2003002281A1
; GENERAL INFORMATION:
; APPLICANT: UONN SIGURD SVENDEN
; APPLICANT: (YSTEIN REXDAL
) APPLICANT: (YSTEIN REXDAL
) APPLICANT: BALDUR SVEINBU (RNSSON
) APPLICANT: LARS VORLAND
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; TITLE OF INVENTION: BIOACTIVE PEPTIDES
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: CTC/GE99/02851
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR FILING DATE: 1998-08-28
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NOS: 30
; SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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1 CFQWKRNMRKV 11
                                                     48 CYGWKRNNKGV 58
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                                                                                                                                                             APPLICANT: MCCATCHY, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2001-03-01
PRIOR PLILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR PLILING DATE: 1998-12-30
PRIOR PLILING DATE: 1998-12-30
PRIOR PLILING DATE: 1999-02-26
PRIOR PAPLICATION NUMBER: 09/259,388
PRIOR PLING DATE: 1999-02-26
PRIOR PAPLICATION NUMBER: 60/122,458
PRIOR PAPLICATION NUMBER: 60/122,458
PRIOR PAPLICATION NUMBER: 60/122,458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-39
PRIOR PILING DATE: 1999-06-39
PRIOR FILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/49,634
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1999-12-29
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PRIOR PILING DATE: 1999-12-29
PRIOR PELING DATE: 2000-02-19
PRIOR PELING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-01
PRIOR PELING DATE: 2000-06-22
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                                   5-09-796-753-26
Sequence 26, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-26
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CTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine CTHER INFORMATION: sequence)
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                                                                                                                       Query Match 53.5%; Score 38; DB 9; Length 15; Best Local Similarity 54.5%; Pred. No. 2.4; Matches 6; Conservative 2; Mismatches 3; Indels
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US-09-798-869-29
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
Sequence 29, USCO030022821A1
GENERAL INFORMATION:
APPLICANT: GUSTEIN REKDAL
SEPLICANT: BALDUK SVEINBURNEN
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
FRIOR APPLICATION NUMBER: PCT/GB99/02851
FRIOR FILING DATE: 1999-08-31
FRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABLOSE FOR Windows Version 4.0
SOFTWARE: FABLOSE FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 45.5
Matches 5; Conservative
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APPLICANT: Desarber, Andrea B.
APPLICANT: Maluli, Khisimuai
APPLICANT: Maluli, Khisimuai
APPLICANT: Bekker, Linda-Gail
APPLICANT: Beker, Linda-Gail
APPLICANT: The Government of the United States of America
APPLICANT: as represented by The Secritetary of the
APPLICANT: as represented by The Secritetary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/889,320
CURRENT FILING DATE: 2000-06-22
PRIOR PELING DATE: 2000-06-24
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, ORGANISM: Mycobacterium tuberculosis
, OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
OTHER INFORMATION: MAP TO AL096701.14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
US-09-864-761-47985
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Pred. No. 59;
2; Mismatches 3; Indels
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               PRIOR FILING DATE: 2001-01:30
PRIOR FILING DATE: 2001-01:30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR FILING DATE: 2001-01:30
PRIOR PILING DATE: 2001-01:30
PRIOR PELICATION NUMBER: PCT/USO1/00670
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 489
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Best Local Similarity 54.5
Matches 6; Conservative
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Pred. No. 2.4;
4; Mismatches
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APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: KYTERN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTUR PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB8818938.4
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAUSEQ FOR WINDOWS VerBion 4.0
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Publication No. US20030022821A1
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   CFRWOWRMKKL 13
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; ORGANISM: BOVINE
US-09-798-869-30
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Search completed: February 21, 2003, 08:11:56 Job time : 6.88372 secs

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Gaps

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lactoferrin - sheep (fragment)
[18cfoferrin - sheep (fragment)
[18cfoferrin - sheep (orientalis aries, Ovis ammon aries (domestic sheep)
[18cfofers 14-Uul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
[18cfofers 14-Uul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
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- Agrobacterium tumefaciens (E) Species: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 (Spacession: H97451 R) R) (Agroession: H97451 R) (Agrobacterium tumefaciens (S) (Agricume S) (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium tumefaciens (Agrobacterium 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A;Experimental source: clone F53H4
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pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A,Map position: A
A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                        Length 708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F53H4.4 - Caenorhabditis elegans
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A;Recession: T22597
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1275 AMILs
A;Residues: 1-275 AMILs
A;Residues: 1
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                                                                                70.4%; Score 50; DB 2; 63.6%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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Pred. No. 0.12;
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                                                                                                                                                                                                                                3; Mismatches
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54.5%;
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Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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R;Accession: JC2223
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: JC2323; MJID:94380047; PMID:8093048
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Reference number: S07160
A;Residues 507160
A;Residues: 436-487, 449-711 (RAD>
A;Residues: 436-487, 449-711 (RAD>
A;Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
B;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A;Reference number: A61169; MUID:9123214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 3421-3423
C;Superfanily: transferrin, transferrin repeat homology
C;Superfanily: transferrin; transferrin iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-71/Product: lactoriansferrin experimental <MAT>
F;20-11/Product: lactoriansferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,171-199,190-201,551-265,530-697,595-609/Disulfide bonds: #status erjs68-800-191,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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A;Residues: 3-701, SWKPVN' <PAN>
A;Residues: 3-701, SWKPVN' <PAN>
A;Residues: 3-701, SWKPVN' <PAN>
B;Residues: 3-701, SWKPVN' <PAN>
B;Residues: 3-701, SWFPVN' <PAN>
B;Residues: 3-701, SWFPVN' <PAN>
B;Residues: 3-701, SWFPVN' <PAN
B;Residues: 3-701, SWFPVN' <PAN
B;Residues: 3-701, SWFPVN' <PAN
B;Residues: 4-701, SWFPVN' <PAN
B;
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A, Molecule type: protein
A, Residues: 20.140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A, Rote: this is the final paper in a series
R, Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Bur. J. Blochem. 241, 303-308, 1996
Bur. J. Blochem. 241, 303-308, 1996
A, Reference number: S74119; MUID:97054624; PMID:8898921
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A,Molecule type: mRNA
A,Residues: 1-708 <LEF>
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication; glycoprotein
F,359-696/Domain: transferrin repeat homology <TRH2>
F,252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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llarity 91.7%; Pred. No. 0.00075;
Conservative 1; Mismatches 0; Indels
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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Best Local Similarity
Matches 11; Conserv
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A,Cross-references: GB:W74778
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
        A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME11517
A;Map position: I
A;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein STY3070 [imported]
                                                                                                                                                                                               Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity
7; Conserve
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A,Molecule type: DNA
A,Residues: 1-511 <PAR>
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I R:Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R.Bazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A,Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A,Reference number: AD3252; PMID:11756688
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A,Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyridoxamine 5'-phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du
C;Species: Agrobacterium tumefaciens
C;Pate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis
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Nolecule type: DNA
Residues: 1-206 «KUR»
(Cross-references: GB.AE008688; PIDN.AAL41776.1; PID:g17739129; GSPDB:GN00186
(Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-208 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
                                                                                                                                                                                                 A,Residues: 1-206 <KUR>
A,Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C;Accession: AG3441
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                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2;
Pred. No. 8.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%; Score 41; DB 58.3%; Pred. No. 8.2; ive 1; Mismatches
                                                                                                                                                                                                                                                                           A;Gene: AGR C 1381
A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
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C,Superfamily: pyridoxamine-phosphate oxidase
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58.3%;
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hes 7, Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 CFHWKSLRROVR 99
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                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
                                                                                                                           A;Accession: H97451
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Matches
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NyAlternate names: lactorraneferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #48quence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41013
B;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Pitele: Lactorraneferrin is the major estrogen inducible protein of mouse uterine secon A;Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyaccession: AB0858
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra A. S.; O'Gaora, P.

Mature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K. A;Atteference number: AB0502; PMID:11677608
A;Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                     - Salmonella enterica subsp. enterica serovar
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A;Gene: STY3070
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A,Residues: 3-707 <-PENA
A,Residues: 3-707 <-PENA
A,Cross-references: EMBL:J03298
R,Liu, Y., Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A,Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A,Reference number: A41205, MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                   C.Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
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Length 208;
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Score 41; DB 2;
Pred. No. 8.3;
1; Mismatches
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Pred. No. 20;
0; Mismatches
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hypothetical protein CPj0126 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar_2001 #sequence_revision 02-Mar_2001 #text_change 02-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A); Cross-references: EMBL:269634; PIDN:CAA93457.1; GSPDB:GN00022; CESP:M18.8 A); Experimental source: clone B0001
R; Steward, C.
Submitted to the EMBL Data Library, January 1996
A; Reference number: Z19800
A; Reference number: Z19800
A; Reference number: Z19800
A; Reference number: Z1999
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-447 cMI2
A; Residues: 1-447 cMI2
A; Residues: EMBL:Z68507; PIDN:CAA92831.1; GSPDB:GN00022; CESP:M18.8
A; Experimental source: clone M18
                                                                                                                                                                                                                                                                            hypothetical protein M18.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T18633; T23799
R;Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, February 1996 A;Reference number: Z18999
A;Accession: T18633
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-447 <WIL>
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Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches
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A;Introns: 41/3; 137/1; 326/3; 434/2
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1852 CFQWQSQLRYIQ 1863
                                      1 CFOWKRNMRKVR 12
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Best Local Similarity
Matches 6; Conserv
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291 WKRNLREV 298
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A;Gene: CESP:M18.8
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, M.J.; Moscola Squame, D.G.; Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc J. Jablc 
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Cypecies: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
Cybate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
Cybatession: 708030
Byhitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Aritle: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Arcession: T08030
A;Arcession: T08030
A;Status: translated from GB/EMBL/DDBJ
A;Arcession: 14568 «MIT>
A;Arcession: 14568 «MIT>
A;Coss-references: EMBL:002963; NID:9409965; PIDN:AAA19956.1; PID:g514215
A;Experimental source: strain 21gr
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A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 348/2; 318/2; 319/3; 1004/3; 1115/3; 3334/3; 388/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 318/2; 31
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F;20-707/Product: lactotransferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 34;
4; Mismatches 3; Indels
                                                                                                                                                                       57.7%; Score 41; DB 1; Length 707; ilarity 54.5%; Pred. No. 28; Conservative 2; Mismatches 3; Indels
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Best Local Similarity 41.7%;
Matches 5; Conservative
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Matches 6; Conserva
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A,Gene: ODA4
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C)Accession: A48396

R)Kruft, V.; Kapp, U.; Wittmann-Liebold, B.

R)Kruft, V.; Kapp, U.; Wittmann-Liebold, B.

R)Aitle: Characterization and primary structure of proteins L28, L33 and L34 from Bacill A; Reference number: A48396; MUD:92075758; PMID:1742360

A; Reference number: A48396

A; Rocassion: A48396

A; Rocassion: A48396

A; Molecule type: protein

A; Rocassion: A48396

A; Molecule type: protein

A; Rocassion: A50 × R03

C; Superfamily: Bscherichia coli ribosomal protein L28
                                                                                                                                                                                                                                                        A,Status: preliminary
A,Ratus: preliminary
A,Rasidus: 1-759 -ARN>
A,Residus: 1-759 -ARN>
A,Cross-references: GB:AE001599, GB:AE001363; NID:g4376387; PIDN:AAD18279.1; PID:g437638
A,Experimental source: strain CWT029
R,Read, T.D.; Brunham, R.C.; Shen, C.; G111, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Mucleic, Acids Res. 28, 1397-1406, 200
A,Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A,Reference number: A81500; MUID:20150255; PMID:10684935
        - Chlamydophila pneumoniae (strains CWL029 and AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 1-759 <REA
A,Cross-references: GB.AE002222; GB.AE002161; NID:G7189553; PIDN:AAF38461.1; PID:g718956
A,Experimental source: strain AR39, HL cells
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Pothetical protein CP0646 [imported] - Chlamydophila pneumoniae (strains of Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Bacillus stearothermophilus
Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 21-Aug-1998
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Pred. No. 66;
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Pred. No. 8.2;
2; Mismatches 1; Indels
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Best Local Similarity 66.7
Matches 6, Conservative
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Best Local Similarity 66.7
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QWKKNLRDV 496
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27 WKANLQKVR 35
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Status: preliminary
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029477 capra hicro

029477 capra hicro

077811 equus cabal

087911 hermoanaer

089565 chlamydomon

098218 drosophila

092372 listeria mo

091187 listeria mo

091187 listeria mo

09187 micopiasma

092372 listeria mo

09187 incorriabdi

021910 caenorhabdi

021910 caenorhabdi

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   (without alignments)
   95.544 Million cell updates/sec
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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CAX2_ARATH
CAX1_ARATH
VP4_ROIGA
PHYC_SORBI
SYB2_RHIME
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Maximum Match 100%
Listing first 45 summaries
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CAEEL
                                                                                                                  OM protein - protein search, using sw model
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HV2ST
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   McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nham M., Parnell L., Dedhia W., Ansaria A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
Sagripanti J.L.,
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
Anderson B.F., Baker H.M., Norits G.E., Rice D.W., Baker E.N.;
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Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 609-711.
MEDLINE-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil
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MEDLINE-88001031; PubMed=3477300;
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comparisons with other transferrins.";
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"Structure of human diferric lactoferrin refined at 2.2-A
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MEDLINE=99190892; PubMed=10089347;
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                       TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
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SEQUENCE OF 3-711 FROM N.A.
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Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUBLLY BICARBONATE (BY SIMILARITY).

-!- SUBCELLIAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameludae; Camelus.
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Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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EMBL; AF156879; AAF82241.1; --
HSSP; O77811; J11X;
InterPro; IRN01156; Transferrin.
Pfam; PF00405; transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SWART; SM00049; TREEK, 2.
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                       Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                        CFOWORNMRKVR 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9838;
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SEQUENCE FROM N.A.
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TISSUS=Mammary gland;
MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=80924 Martin P.;
MICHARACTERIZATION of the goat lactoferrin cDNA. Assignment of the relevant locus to bowine U12 syntemy group.";
MICHARACTERIZATION SECTEMBRAINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
--- SUBUNIT: MONOMER (BY SIMILARITY).
--- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                     Capra hircus (Goat).
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
                                     .
70.4%; Score 50; DB 1; Length 708; 66.7%; Pred. No. 0.22; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Nammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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695 AA

PRT;

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                   SEQUENCE FROM N.A.
Paramestvam M., Srinivasan A., Yadav M.P., Singh T.P.;
Paramestvam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
"Lumitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lacrotransferrin precursor (Lacroferrin) (Fragment).
                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                 Equus caballus (Horse)
                                      TRFL HORSE
077811;
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                             EMBL; U53857; AAA97958.1; -.
EMBL; X7802; CAA55517.1; -.
EMBL; X7802; CAA55517.1; -.
EMBL; X7802; CAA55517.1; -.
EMBL; X7802; CAA55517.1; -.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
EMART; SM00494; TR FER, 2.
PROSTTE; PS00206; TRANSFERRIN. 2; 2.
PROSTTE; PS00206; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 50; DB 1; Length 708; llarity 63.6%; Pred. No. 0.22; Conservative 3; Mismatches 1; Indels
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L -> R (IN REF. 2).
F -> F (IN REF. 2).
F -> P (IN REF. 2).
S -> R (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C83539960D CRC64;
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IRON 4 (BY SIMILARITY).
ANION (BY SIMILARITY).
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                              BY SIMILARITY.
LACTOTRANSFERRIN.
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                                                                                                            resolution.";
J. Mol. Biol. 289:303-317 (1999).
-I- FUNCTION. TRANSFERRINS ARE IRON BINDING TRANSPORT PROFEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ010930; CAA09407.1; -.

R PDB; 1B1X; 02-DEC-98.

R PDB; 1B7X; 02-EEB-99.

R PDB; 1B7X; TRANSFERRIN.

R PROSTITE; PS00205; TRANSFERRIN 1; 2.

R PROSTITE; PS00205; TRANSFERRIN 1; 2.

R PROSTITE; PS00207; TRANSFERRIN 3; 1.

T Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Transferring 1.

T SIGNAL <-1 6
                                                   Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P. "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                       -i- SUBUNIT: MONOMER.
-i- SUBCELLUTAR LOCATION: Secreted.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOWAINS.
-i- SUMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACTOTRANSFERRIN
TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
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                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MB4 / JCM 11007;
MEDLINE-21992816; PubMed=11997336;
Bao (D. Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yan Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., I Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:669-700(2002).
                                                                                                                                                                                                                                                                                     59.2%; Score 42; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 62;
Pred, No. 0.69;
                                                                                                                                                                                                                                                                                                                1; Indels
                                                                              IRON 1 (BY SIMILARITY).
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N-LINKED (GLCNAC. . ) (F
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Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AA.
                                                                                                                                                                                                                                                                                                Pred. No. 5.7;
4; Mismatches
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70.0%;
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Best Local Similarity 58.3
Matches 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                       25 CAKFQRNMKKVR 36
                                                                                                                                                                                                                                                                                                                                        1 CFQWKRNMRKVR 12
 NCBI_TaxID=119072;
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3 QWKRNMRKVR 12 :|| |:|||| 27 RWKPNIRKVR 36

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-14 FROM N.A.

MEDLINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991).

-I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.

-I- SUBUNIT: MONOMER.
                                                                                                                                                                                                                                MEDLINE=87280033; PubMed=3611056; Pentecost B.T., Teng C.T.; "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                      Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLUTAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
TRFL_MOUSE STANDARD; PRT; 707 AA. P08071; P7059; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) PL-UNX-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN.
1.
                                                                                                                                                                                                                                                                                                  Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001156; Transferrin.
Pfau, PR00405; transferrin;
PRNUTS; PR00422; TRANSFERIN;
SMART; SM00094; TR_FER; 2.
PROSITE; PR00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, J03299; AAA40525.1; -.
EMBL, D88510; BAA13633.1; -.
EMBL; BC006904; AAA406904.1; -.
EMBL; M74779; AAA3427.1; -.
PIR; A28439; A28438.
HSSP; P02788; LCE6.
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357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILA DROME STANDARD; PRT; 292 AA.

09XZLB; Q9V391;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2000 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nebula protein.
NILA OR CG6072.
Drosophila melanogaster (Fruit fly).
Briscycta; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Nuscomorpha; Ephydroidea; Drosophila.

NISH TAXID-7227;
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MEDLINE=20196006, PubMed=10731132;
Adams M.D., Celniker S.B., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Bananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
Abrill J.F., Agbayani A., An Andrews-Pfannkoof C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaeley B.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
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COLLED COLL (POTENTIAL).
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MICKOTUBLIES BINDING (POTENTIAL).
MICKOTUBLIES BINDING (POTENTIAL).
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Pred. No. 92;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                             EMBL; U02963; AAA19956.1; -.
InterPro; IPR04273; Dynain heavy.
Pfan; PP03028; Dynein heavy. 1.
Motor proțein; Microtubules; Dynein; ATP-binding; Flagella;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Best Local Similarity 41.7°,
Best Local Similarity 5, Conservative
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1852 CFQWQSQLRYIQ 1863
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SEQUENCE
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NLA_DROME
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J. Cell SCA. 107:615-644(1994).
J. Cell SCA. 107:655-644(1994).

-1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

PUNEIN HAS AFRARE ACTIVITY.

-1- SUBDNIT: CONSIGTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
SEQUENCE 3427478; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
MR -> IQG (IN REF. 1).
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S -> I (IN REF. 2).

S -> T (IN REF. 2).

A -> D (IN REF. 1).

E -> G (IN REF. 1).

L -> V (IN REF. 1).

L -> V (IN REF. 1).
  2.
BY SIMILARITY.
IRON 1 (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
0DA4 OR ODA-4 OR SUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1
Pred. No. 8.7;
2; Mismatches
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77865 MW;
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Best Local Similarity 54.3%,
Best Local Similarity 64.3%,
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DYHB_CHLRE
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!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS
             -!- SIMILARITY: BELONGS TO THE L28P F.
FIR; A48396; A48396.
INTERPTO; IPRO01383; Ribosomal L28.
FEan; PRO0830; Ribosomal L28.
TIGRFAMS; TIGRO0009; L28; 1.
Ribosomal protein.

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SEQUENCE

60 AA; 6810 MW; ZAD9161C]
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EMBL; AL596170; CAS97160.1; -.
Listilist; LIN01930; -.
Listilist; LM001816; -.
InterPro; IPR001381; Ribosomal L28.
Pfam; PF00830; Ribosomal L28.
TGRFAMB; TISRO0009; L28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                  53.5%;
                                                                                                                                                                                                        Cuery Match
Query Match
Best Local Similarity 66.77,
Best Local Similarity 65.77,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Listeria monocytogenes, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50S ribosomal protein L28. RPMB OR LMO1816 OR LIN1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1639, 1642;
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                  4 WKRNMRKVR 12
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Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

A Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P.,

A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

B Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelister C.C., Ferriers S., Felsischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

A Harris N.L., Harvard C.F., Hermandez J.R., Houck J.,

RA Harris N.L., Harvard T.J., Hermandez J.R., Houck J.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

A Lakko P., Lei Y. Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lakko P., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

A Lakko P., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lakko P., Lei Y. Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Muzphy L., Marny D.M., Nelson D.L.,

RA Rahnert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Rahnert K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho X., Smith H.O.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Venter J. C.,

RA Globs R.A., Myers B.W., Rubin G.M., Weissenback J. C.,

RA Globs R.A., Wasser B.W., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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Kruft V., Kapp U., Wittmann-Liebold B.;
Characterization and primary structure of proteins L28, L33 and L34
from Bacillus stearothermophilus ribosomes.";
Biochimie 73:855-860(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.9%; Score 39; DB 1; Length 292; 54.5%; Pred. No. 7.9; 2; Indels tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBGD0026629; nla.
292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
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NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus.
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Best Local Similarity
6; Conserve
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P23374;
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SEQUENCE
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Glaser P., Frangeul L., Buchisser C., Rusniok C., Amend A.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Deboux P.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dushoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dusurget O.,
A Brian K.-D., Fshii H., Garcia-del Portillo F., Garrido P.,
Gautier L., Gebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Raerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mara Vicente J., Ng E., Nedjari H.,
Nordaise G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
"Comparative genomics of Listeria species.",
Is Science 294:849-852[2001).
L. SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                     Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGRODOUS; LLCO, LIGHT Ribosomal protein; Complete proteome.
TIGRFAMS; 6991 MW; AA43DE039213C562 CRC64;
60 AA; 6810 MW; 2AD9161CD60E82F4 CRC64;
                                                                 Score 38; DB 1;
Pred. No. 2.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.5%; Score 38; DB 1; 66.7%; Pred. No. 2.3; iive 2; Mismatches
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HIV; X14307; VIF$SMMH4.
InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                  267 AA; 30425 MW;
                                                                                                                                                                                                                                                                  EMBL; Z33006; CAA83689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X14307; CAA32484.1; -. PIR; S07989; S07989.
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 CFGKKENMRQMR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWKRNMRKVR 12
NCBI_TaxID=2095;
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                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                     rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
                                                                                                                                                                                                                                                                             Planet P., Jagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                            {RNA}(N).
-1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan, PF00562; RNA pol B; 1.
PROSITE; PS01166; RNA POL BETA; PARTIAL.
Transferase; Transcription; DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Hypothetical protein (Fragment).
Mycoplasma capricolum.
Macoplasma repricolum.
Entomoplasmataceae.
                                                                                                                                                                                          Liberibacter africanus (Liberobacter africanum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001572; RNA_pol_B.
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les 6; Conservative
                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWKRNMRK 10
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  4 WKRNMRKVR 12
                        29 WKANLOKVR 37
                                                                                                                                                                                                                                                                     STRAIN=Nelspruit;
                                                                                                                                                                                                                              NCBI_TaxID=34020;
                                                                                        RPOB LIBAF
P41187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYCCA
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SEQUENCE
                                                                                                                                                                                                                                                      SEQUENCE
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P53661;
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Y125_MYCCA
DD Y125_MY
AC P53661,
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
DT 01-0CT-
OS MYCOPI,
OS MYCOPI,
OS EACCETI
                                                             RESULT 11
RPOB_LIBAF
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIR=ATCC 27434 / KID;
MEDLINE=SEO59641; PubMed=7476192;
BOTK P., Ouzounis C., Casari G., Schneider R., Sander C.,
Bolan M., Gilbert W., Gillevet P.M.;
"Exploring the Mycoplasma capticolum genome: a minimal cell reveals its physiology.";
Mol. Microbiol. 16:955-967(1995).
-! SIMILARITY: BELONGS TO THE COF/YEHA/YIDA/YIGL (E.COLI) / YCSE/YXEH (B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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NCBI_TaxID=11737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "An African rimate lentivirus (SIVsm) closely related to HIV-2."; Nature 339:389-392(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.5%; Score 38; DB 1; Length 267; 58.3%; Pred. No. 11;
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MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D5912DD5B39A8451 CRC64;
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Virion infectivity factor (SOR protein) (Q protein).
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01-077-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update
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InterPro; IPR000150; Hypothet_cof.
Pfam; PF00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
Hypothetical protein.
267
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[1] SEQUENCE FROM N.A. (A*3401/A*3402).
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EMBL; X61705; CAA43874.1; -.
PIR; S16767; S16767.
PIR; S16771; HSSP; O19673; 1HSB.
MIM; 142800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC I; 1.
Probon; PD000050; MHC I; 1.
SWART; SW00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003006; 19 MHC.
InterPro; IPR003597; 19_c1.
InterPro; IPR001039; MHC_I.
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                                                                                                   NCBI_TaxID=9606;
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115
207
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TRANSMEM
DOMAIN
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DISULFID
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _1A34_HUMAN STANDARD, PRT; 365 AA.
P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- COFACTÓR: FAD (POTENTIAL).
-i- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                   Score 37; DB 1; Length 214; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 37; DB 1; Length 783; 50.0%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BMBL; Z35602; CAA84471.2; -.
WormPep; R13G10.2; CE25088.
InterFor: IPR002937; Amino. oxidase.
Pfam; PF01593; Amino. oxidase; 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD.
Hypothetical, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Durbin R.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                214 AA; 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
873G10.2.
                                                                                                                                                                                                                                                                                                                                 783 AA
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                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                 PRT;
Pfam; PF00559; V1f; 1.
PRINTS; PR00349; VIRIONINFPCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                   52.1%;
75.0%;
                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                  170 ÓWRRINNRK 177
                                                                                                                                                                                              3 QWKRNMRK 10
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                                                                              SEQUENCE
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ID 1A34 H1

AC P30453,
DT 01-APR

DT 16-OCT-
DE HLA Cle
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYMIL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (A*3401/A*3402).
SEQUENCE FROM N.A. (A*3401/A*3402).
MEDINE=9323511; PubMed=8475492;
Madrigal U.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-Al0 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-34(A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .) (BY SIMILARITY)
                                                                                                                                                                                                                                                                       MEDLINE=93056508; PubMed=1431115; Madrigal U.A., Belich M.P., Hildebrand W.H., Benjamin R.J., Madrigal U.A., Zemmour U., Ennis P.D., Ward F.E., Petzl-Erler M.L., Martell R.W., du Toit E.D., Parham P.; Distinctive HiA-A,B antigens of black populations formed by interallelic conversion ": J Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401
(AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
precursor.
Hia-A OK HiaA.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with serology.";
Tissue Antigens 41:72-80(1993)
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Signal; Polymorphism.
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EXTRACELLULAR ALPHA-3.
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FTId=VAR 00479.

K -> N (IN A*3402).

FTId=VAR 004380.

R -> I (IN A*3402).

FTId=VAR_004381.
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BY SIMILARITY.
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								CRC64;
P -> S (IN A*3402).	/FTIG=VAR_004382.	Q -> R (IN A*3402)	/FTIG=VAR 004383.	W -> L (IN A*3402)	/FTId=VAR 004384.	L -> I (IN A*3402)		MW; 063BF63E6E6E01F6
129		138		180		312		41055
129		138		180		312		365 AA; 41055
VARIANT		VARIANT		VARIANT		VARIANT		SEQUENCE
E.	FT	FT	FT	FŢ	ŦŦ	Ľы	H	ÖS

Query Match
 50.7%;
 Score 36;
 DB 1;
 Length 365;

 Best Local Similarity 66.7%;
 Pred. No. 34;
 Mismatches
 2;
 Indels

 Matches 6;
 Conservative 1;
 1;
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 4 WRNMRKVR 12
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 84 WDRNTRKVW 92
 3
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0; Gaps

Search completed: February 21, 2003, 07:51:39 Job time : 6.2093 secs

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Q9jjzs mus musculu Q9sjjzs mus musculu Q9z85s chlamydia p Q9z85s chlamydia p Q8srg3 encephalito Q8srg4 encephalito Q90884 human immun Q77855 human immun Q77855 human immun Q9sml2 cicer ariet Q6sml1 cicer ariet Q6srg4 horseradish Q8yp77 anabaens sp Q8rax2 homo sapien Q9ffy4 salmonella Q8fza4 mus musculu Q8f53 hemerocalli Q9ztp0 cyrza sativ Q9ztp0 cyrza sativ Q25f11 helicobacte
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Q9ftt0 oryza sativ
Q8s487 zea mays (m
O81437 arabidopsis
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Ogwld5 drosophila
Ogfhig arabidopsis
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Q9nus2 homo sapien
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 017549 caenorhabdi
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogucys;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Home sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.3%; Score 62; DB 4; Length 711; 90.9%; Pred. No. 0.0074; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. Submitted (FEB-2002) to the EMBL; EC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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017549
094JZS
092955
062862
08884
090884
077855
09XKDS
098ML2
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Q8YP77
Q8TAX2
Q9F7Y4
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Q9NUS2
P96223
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09W1D5
09FHI9
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Q9ZTP0
Q25611
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Q9FTT0
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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TISSUE=PROSTATE;
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Lactotransferrin.
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Matches
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Q8TCD2
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Q879u thermoanaer
Q886a rhizobium 1
Q84k3 brucella me
Q87k3 brucella me
Q87k3 brucella me
Q87k5 salmonella
Q97kp1 sesamum ind
Q97kp1 sesamum ind
Q97kp1 homo sapien
Q91kp3 halobacteri
Q91kp3 halobacteri
Q91kg rhizobium 1
Q8xse2 ralstonia s
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Osucy5 homo sapien
Ostr80 ovis aries
O93780 caenorhabdi
                                                                                                  February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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            GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     protein search, using sw model
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Q9UCY5
Q9UCY5
Q93780
Q93780
Q8R9U1
Q9BGAQ
Q9ZRH8
Q8ZFG
Q9ZRH8
Q8ZFG
Q9ZRH9
Q9ZRPI
Q9GM21
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Q8XSE2
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sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_invertebrate:*
sp_mammal:*
sp_mho:*
sp_phage:*
sp_plant:*
sp_vordent:*
sp_virus:*
sp_virus:*
sp_virus:*
sp_vortebrate:*
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
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Match Length DB
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBL_TaxID=119072;
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N SEQUENCE FROM N.A.
CSTRAIN-MB4T / JCM11007;
RX MEDLINE=21992816; FubMed=11997336;
RX MEDLINE=21992816; FubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lang H.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RA Genome Res. 12:689-700(2002).
RI Genome Res. 12:689-700(2002).
DE EMBI; AR013107; APM24713.1; -.
Chanlate proteome. 7027 MW; CAADB605C81D495D CRC64;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
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Kanako T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 16; Length 62;
Pred. No. 3.6;
2; Mismatches 1; Indels
                                                       "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                   r Match 63.4%; Score 45; DB 5; Length 275; Local Similarity 72.7%; Pred. No. 3.1; es 8; Conservative 1; Mismatches 2; Indels
                                                                       investigating biology;";
Science 282:2012-2018[1998].
EMBL; Z81089; CAS03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UTM-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
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SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermoanaerobacter tengcongensis.
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70.08;
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                      262 FOWKISMRKTR 272
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                            "Characterization of the 84-kDa protein with ABH activity in human
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                  81.7%; Score 58; DB 4; Length 38; 90.9%; Pred. No. 0.0019;
                                                                                                                                                                                                                                                                                                        0; Indels
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
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MEDIANE=5127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
HSCP, O77698; LCE2.
InterPro; IPRO01156; Transferrin.
Fran; PG00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MM; D1904CAE15A73961 CRC64;
                                                                                                                                                                                    InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fragment).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                            seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; lBKA.
                                                 SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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01-FEB-1997 (TrEMBLrel, 02,
01-AUG-1998 (TrEMBLrel, 07,
01-DEC-2001 (TrEMBLrel, 19,
F3H4.4 protein.
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Matches 6; Conservative
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Matches 10; Conserv
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                  NCBI_TaxID=9606;
                                                                                          Sato I.;
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1 CFQWKRNMRKVR 12
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Best Local Similarity
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SEQUENCE
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Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
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"The genome of the natural genetic engineer Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21608550; PubMed=11743193; Monks D.E., Kitajima J.P., Okura V.K., Zatubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chen Y., Paulsen I.T., Datherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Krespan W., Perry M., Ghumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
Pyridoxamine 5'-phosphate oxidase.
PAGROBACTERIUM tumefaciens (strain CS8 / ATCC 33970).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group,
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"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
                                                                                                                                                                                                                            57.7%; Score 41; DB 16; Length 205; 58.3%; Pred. No. 12; 4; Indels iive 1; Mismatches 4; Indels
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                                                                                                                                                                                            205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
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                                                                            EMB1, AP003011, BAB53553.1; -.
InterPro, IRR000659; Pyridox oxidase.
Fram, PP01243; Pyridox oxidase, 1.
ProDom; PD006312; Pyridox oxidase; 1.
TIGRFAME; TIGR00558; pdxH; 1.
COMD1ET; PS01064; PYRIDOX_OXIDASE; 1.
COMD1ETE; PC01064; PYRIDOX_OXIDASE; 1.
SEQUENCE 205 AA; 23300 WW; 0BADE4CD3
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MEDLINE=21608551; PubMed=11743194;
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                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.3
Matches 7; Conservative
                                                  Mesorhizobium loti.";
DNA Res.'7:331-338(2000)
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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Best Local Similarity
Matches 7; Conserv
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A Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
B boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
A Codrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Codrie T., Goffeau A., Purnelle B., Ramsperger U.,
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
Analysis of the chromosome sequence of the legume symbiont
I Analysis of the chromosome sequence of the legume symbiont
I Sinorhizobium meliloti strain 1021.";
Froc. Natl. Acad. Sci. U.S.A. 98:9977-9882 (2001).
B EMBL; AL591785; CAC45467.1;
B FMBL; AL591785; Pyridox oxidase.
R Probom; PF001243; Pyridox oxidase; 1.
Probom; PF01243; Pyridox oxidase; 1.
PRODOM; PF0164; PYRIDOX OXIDASE; UNKNOWN_1.
OXIGOTEABLE PYRIDOX OXIDASE; UNKNOWN_1.
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MEDLINE=20020109; PubMed=11756688;
DelVecchio V. G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
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PDXH OR R00895 OR SMC00069.
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria, Proteobacteria, alpha subdivision; Rhizobiaceae group;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WM-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
BMEI1517.
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Pred. No. 12;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                     206 AA.
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                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
88 CFHWKSLRROVR 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWKRNMRKVR 12
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RESULT 10 Q8Z462

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SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed storage proteins in sesame.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2S albumin.
Sesamum indicum (Oriental sesame) (Gingelly).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
                         STRAIN=NUSI82; Barndel W.K., Janssens W., Adu-Sarkodie Y., Aparadel J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y., Apagogyei F., Anyomi F., Aidoo S., Barnor J.S., Yamamoto N., Ishikawa K., Sata T., Kurata T.; "Genetic and phylogenetic analysis of HIV-1 strains from Southern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.3%; Score 40; DB 10; Length 148; 66.7%; Pred. No. 13; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 15; Length 81;
Pred. No. 7.1;
2; Mismatches 1; Indels
                                                                                                                                                                                                         Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225659; CAA12541.1; -. Interprey, IPROOF77; GP120. Pfam: PP00516; GP120; J. AIDS; Coat protein; Glycoprotein.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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EMBL; AF091841; AAD42943.1; -.
Interpro; IPR0005612; AAI.
Interpro; IPR000617; Napin.
Interpro; IPR00017; Napin.
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01-DEC-2001 (TrEMBLrel. 19, Last seque)
01-DEC-2001 (TrEMBLrel. 19, Last anno
CDAR FLJ22891 fis, clone TESTI2004929
FOMO SAPAGENS (Human).
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PRINTS; PR00496; NAPIN.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.3%;
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es 6; Conservative
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nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QWKRNMRKV 11
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54 CMQWMRSMR
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SEQUENCE
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Q96M21
ID Q96M2
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AC Q96M2
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DT 01-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                       57.7%; Score 41; DB 16; Length 208; 58.3%; Pred. No. 12; ive 1; Mismatches 4; Indels
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009587; AAL52698.1; -.
InterPro; IPR00659; Pyridox_oxidase.
Pfam; PF0143; Pyridox oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
ProDom; PD006312; Pyridox_oxidase; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
Oxidoreductase; Complete proteome.
SEQUENCE 208 AA; 23866 MW; CBIF50BC9612DBZ8 CRC64;
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EMBL, AL627276; CAD06049.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01ycoprotein gpl20 (Fragment).
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                           Local Similarity 58.3
es 7; Conservative
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Matches 7; Conservative
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Search completed: February 21, 2003, 08:00:45 Job time : 22.6744 secs
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MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed=11016950;
MEDLINE-20504483; PubMed-2050; Medli R., Gao M., Gao M., Calar K., Cruz R., Danson M.J., Hough D.W.,
Meddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Meddocks D.G., Jablonski P.E., Krebs M.P., Spudich J.L., Jung K.-H.,
Meddocks D.G., Jablonski P.E., Dohlschroder M., Spudich J.L., Jung K.-H.,
M. Senbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
M. Senbardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
M. Genome sequence of Halobacterium species NRC-1.";
MEDLIA Acad. Sci. U.S.A. 97:12176-12181(2000).
M. EMBL, ABGO1646; Speptide repeat.
M. InterPro: IPRO01646; Speptide repeat.
M. Grouplete proteomentapptide, Z.
M. Groplete M. M. J. M. 
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                                                                                                                                                               SECUENCE FROM N.A.

TISSUB-TESTIS;
Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekime M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
'NEDO human DNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOS7453; BAB71493.1;
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SEQUENCE 274 AA; 30083 MW; IDD43654D4135B2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 56.3%; Score 40; DB 4; Length 274; Local Similarity 50.0%; Pred. No. 25; les 6; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNĞ1732C,
Halobacterium sp. (strain NRC-1).
Archaea; Buryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
NCBI_TaxID=64091;
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Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                    NCBI_TaxID=9606;
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031090
ID 031090
AC 031090;
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Matches
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Gaps
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            01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae)
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                         MEDLINE=99113394; PubMed=9914965;
Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G.
Ksenzenko V.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                    54.9%; Score 39; DB 2; Length 273; 60.0%; Pred. No. 37; 1; Indels 1; Indels
                                                                                                                                                             STRAIN=VF39;
Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N
Inditted (CCT-1997) to the EMBI/Genbank/DDBJ databases:
                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
 01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity (
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                                                                                                                                              SEQUENCE FROM N.A.
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WPI; 2000-147388/13.
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                                                                                           February 21, 2003, 07:37:21; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                 OM protein - protein search, using sw model
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AAY78038
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AAY78046
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AAY78092
AAY78089
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Gapop 10.0 , Gapext 0.5
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1 AAY7808 1 AAY7809 1 AAY7803 1 AAY7804 1 AAY7804	\( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \) \( \cup \)	7 AAR985 7 AAR918
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## ALIGNMENTS

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dolphin GT;
                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L,
                                         AAY78093 standard; Peptide; 12 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-SE01230.
                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                      WO20001730-A1.
                                                                                                                                                                                                                                                                                                            Homo sapiens.
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29-DEC-1998;
                                                                                                                      25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                             13-JAN-2000.
                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                               AAY78093;
RESULT 1
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fin food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                         anti-inflammatory auti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:74.
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                                                                   Claim 22; Page 38; 102pp; English.
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29-DEC-1998;
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Dolphin GT

Baltzer L,

Mattsby-Baltzer I,

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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Dactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant foomlula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, lactoferrin, modification; infection, inflammation, tumour;
food, infant formula, anti-inflammatory, anti-miorobial, anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                          Score 65; DB 21; Length 12; Pred. No. 0.00019; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:91.
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9888-0002562.
9888-0004614.
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91.7%;
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29-DEC-1998;
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Gaps .; 0

100.0%; Score 69; DB 21; Length 12; 100.0%; Pred. No. 4.2e-05; ive 0; Mismatches 0; Indels

12 AA;

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Gaps

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Score 63; DB 21; Length 12; Pred. No. 0.00042; 0; Mismatches 1; Indels

12 AA;

Sequence

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12 AA;
                                                                  WO200001730-A1
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17-JUL-1998;
29-DEC-1998;
                                                            sapiens
                                                                           06-JUL-1999;
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                                                                                              Hanson LA,
                                                             Synthetic
Sequence
                                  AAY78092;
                        ESULT 4
AY78092
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Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.

Human lactoferrin derived peptide SEQ ID NO:89.

(first entry)

25-APR-2000

AAY78089;

AAY78089 standard; Peptide; 12 AA.

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Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                     Score 63, DB 21, Length 12, Pred. No. 0.00042, 0, Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative (
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98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1

Homo sapiens.

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unimary tract infections, colitis, and candida infection on a mucosal unimary tract inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used on the peptides can also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower can be compared to the same purposes as lactoferrin at lower.
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                                                                       Dolphin GT
                                                                           Baltzer L,
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                                                                           Hanson LA, Mattsby-Baltzer I,
(ASCI-) A+ SCI INVEST AB.
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Best Local Similarity
Matches 10; Conserva
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RESULT

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Human lactoferrin derived peptide SEQ ID NO:86.
AAY78086 standard; Peptide; 12 AA.
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98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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29-DEC-1998;
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                                                                                                                                                                                                                                                             Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection, colltis, Candida infection, fungicidal;
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                                                                                                                       AAY78090 standard; Peptide; 12 AA.
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98SE-0002562.
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1 CFOWKRAMRKVR 12
                     1 CFQWQRXMRKVR 12
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Best Local Similarity
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17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrans), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                               food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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duman; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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83.3%; Pred. No. 0.0013;
tive 1; Mismatches 1; Indels
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as urinary tract infearins and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Byon though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would be enable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Best Local Similarity 83.3%;
Matches 10; Conservative
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29-DEC-1998;
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Dolphin GT;

98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the direction. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections and/or prevention of infections (such as uniform and/or tumours. The peptides can also be used membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also thungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                     of infections,
formula food
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Pred. No. 0.002;
1; Mismatches 1; Indels
                                                                                                                                                                                                                       Dolphin GT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78047 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
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Best Local Similarity 83.3
Matches 10; Conservative
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29-DEC-1998;
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 Synthetic.
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Score 59; DB 21; Length 12; Pred. No. 0.002; 1; Mismatches 1; Indel8

12 AA;

1; Mismatches

(first entry)

Baltzer L,

98SE-0002441. 98SE-0002562. 98SE-0004614.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through beinding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections (such as medosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used on though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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                                                                                                                                                                                                      New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                       Claim 18; Page 73; 102pp; English
                                                                                                                            Hanson LA, Mattsby-Baltzer I,
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                                                                                  (ASCI-) A+ SCI INVEST AB
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06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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Matches
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98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through confiding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unimary tract infections, colitis, and candida infections on a musosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used as preservatives. The peptides are also anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used claimically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
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Dolphin GT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
 Baltzer L,
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                                                                                                                  Claim 22; Page 36; 102pp; English.
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 Hanson LA, Mattsby-Baltzer I,
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98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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29-DEC-1998;
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85.5%; Score 59; DB 21; Length 12; 83.3%; Pred. No. 0.002; 1; Mismatches 1; Indels

12 AA;

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13 AA;
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29-DEC-1998;
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                                       AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections a mucosal membrane), inflammations and/or tumours. The peptides can also be used to fund and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 0.002;
1; Mismatches 1; Indels
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Claim 22; Page 38; 102pp; English.
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98SE-0002562.
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Best Local Similarity
Matches 10; Conserv
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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           membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection; colitis; Candida infection, fungicidal;
bactericidal, preservative.
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colitis, and Candida infection on
                                                                                                                                                                                                                                                                                        85.5%; Score 59; DB 21; Length 13; 83.3%; Pred. No. 0.0021; ive 1; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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les 10; Conservative
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costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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13 AA; Sequence

.. 0 Gaps ö Query Match 85.5%; Score 59; DB 21; Length 13; Best Local Similarity 83.3%; Pred. No. 0.0021; Matches 10; Conservative 1; Mismatches 1; Indels

1 CFOWKRAMRKVR 12

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2 CPOWORNWRKVR 13

RESULT 15 AAY78049

AAY78049 standard; Peptide; 13 AA.

AAY78049;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:49.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumo urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens. Synthetic.

13-JAN-2000

WO200001730-A1.

99WO-SE01230. 06-JUL-1999;

98SE-0002441. 98SE-0002562. 98SE-0004614. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

(ASCI-) A+ SCI INVEST AB.

Baltzer L, Mattsby-Baltzer I, Hanson LA,

Dolphin GT;

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 74; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract inflections, colitis, and candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used allocated based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

13 AA;

85.5%; Score 59; DB 21; Length 13;

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83.3%; Pred. No. 0.0021;
tive 1; Mismatches 1; Indels
Best Local Similarity 83.3
Matches 10; Conservative
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2 CFQWQRNMRKVR 13

Search completed: February 21, 2003, 07:56:44 Job time : 28.093 secs

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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICKARI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: VENDENCEN: INTERTION: INTERTION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATERY ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
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LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
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STATE: MA

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC COMPATIBLE

COMPUTER: BEACHILL

COMPUTER: DALCHILL

ATTORNEY AGENT INFORMATION:

CAMPBELL, PAULA A.

REFERENCE/DOCKET NUMBER: PJN-019

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO:

SEQUENCE: CAMPACTERISTICS:

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Patent No. 5565425
GENERAL INFORMATION:
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                                                                                                                                                               February 21, 2003, 07:50:40; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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1. /cgn2 = /ptodata1/liaa/5A COMB.pep:*

2. /cgn2 = /ptodata1/liaa/5B COMB.pep:*

3. /cgn2 = /ptodata1/liaa/6A COMB.pep:*

3. /cgn2 = /ptodata1/liaa/6B COMB.pep:*

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5. /cgn2 = /ptodata1/liaa/PCTUS COMB.pep:*

6. /cgn2 = /ptodata1/liaa/PCTUS COMB.pep:*
                       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-26-771-25

US-08-26-771-25

US-08-381-984-24

US-08-381-984-24

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Listing first 45 summaries
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APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERARA
TITLE OF INVENTION: AND METHODS OF THEIR USE
TITLE OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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Pred. No. 0.0015;
1; Mismatches 1; Indels
                                                                                                                      85.5%; Score 59; DB 1; Length 18; 83.3%; Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: Use
ZIP: 07601
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                         1; Mismatches
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CLASSIFICATION: 436
PILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLIL 7, 1995
CLASSIFICATION: 436
ATTOREY/ABENT INFORMATION:
NAME: JACKSON TOWNERR: 26,742
REGISTRATION NUMBER: 36,742
REGISTRATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-485-948-8; Sequence 8: Application US/08485948; Patent No. 585582; GENERAL INFORMATION:
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                                                                             Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                            1 CFQWKRAMRKVR 12
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CFCWQRNMRKVR 12

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                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: UL, YONG
APPLICANT: UL, YONG
APPLICANT: CERAMI, ANTHONY
APPLICANT: CERAMI, ANTHONY
APPLICANT: CERAMI, ANTHONY
APPLICANT: CERAMI, ANTHONY
APPLICANT: CERAMI, ANTHONY
APPLICANT: CERAMI, ANTHONY
NUMBER OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF INVENTION: AGE-MEDIATED
NUMBER OF SEQUENCES:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
CONTEX: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08475055
Patent No. 5962245
GENERAL INPORMATION:
APPLICANT: YOUNG LI
APPLICANT: ANTHONY CERAMI
ITILE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ABDPRODUCTS; AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                            Score 59; DB 2;
Pred. No. 0.0015;
1; Mismatches
Sequence 8, Application US/08628380 Patent No. 5891341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 201 343-1684
TELEX: 133521
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWKRAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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FEATURE:
NAME/KEY:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Liol group of OTHER INFORMATION: thiol group of CYBE INFORMATION: PUBLICATION THIOR PUBLICATION: PUBLICATION THIOR PUBLICATION THIOR PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLICATION TO THE PUBLIC
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 20;
                               SOFTWARE: Displaywite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%; Score 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WATTEN M. Cheek JT.
REGIGSTRATION UNUMBER: 33,367
REFRENCE/DOCKET NUMBER: 33,367
RELEFRANCE/DOCKET NUMBER: 31,267
TELEFOMMUNICATION INFORMATION:
TELEFROMMUNICATION 100.371-8856
TELEFAX: 202-371-8856
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NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
PRACHENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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CLONE:
CLONE:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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DOCUMENT NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.5%; Score 59; DB 2; Length 18; 83.3%; Pred. No. 0.0015; Live 1; Mismatches 1; Indels
                      ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
STAIE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER: Eloppy disk
COMPUTER: Pachalle FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Pachalle FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: Pachalle FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: Pachalle FORM:
MEDIUM TYPE: Plopy disk
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: Pachalle Rolease #1.0, Version #1.25
COMPUTER: David A.
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Accison 88q., 1995
CLASSIFICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REBERRICE/OPCKET WUMBER: 26,742
REBERRICE/OPCKET WUMBER: 2014487-5800
TELEPRAK: 2014487-5800
TELEPRAK: 201343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/07755161A
Patent No: 5304633
GENERAL INFORMATION:
APPLICATY: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Wanderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005 COMPUTER READBLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201343-1684
FELEX: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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FRAGMENT TYPE: internal
S-08-475-055-8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWKRAMRKVR 12
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DEMILITARIES INFORMATION: (note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
FERTURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: 19
OTHER INFORMATION: (note= "thiol group of OTHER INFORMATION: (riol group of OTHER INFORMATION: thiol group of Cys residue at location 2" sulfide bond with PUBLICATION INFORMATION: AUTHORS.
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APPLICANT: NAKAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANABAKI, YOSHIHIRO
APPLICANT: TANABAKI, YOSHIHIRO
APPLICANT: TUTLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEGUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REPERENUE/POCKET NUMBER: FJN-019
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.5%; Score 59; DB 1;
Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08204487 Patent No. 5565425 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWKRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
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                                       ó
                                       Gaps
                                       1; Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
    TITLE OF INVENTION:
    TITLE OF INVENTION: Antimicrobial Peptides and an ITILE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
    CITY: Washington
    STATE: D.C.
Pred. No. 0.0016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM COMPALIBLE
OVERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERRINGE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELESPACE: 202-371-8856
FILIEDRAX: 202-371-8856
                                   1; Mismatches
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
IENGTH: 20 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified site
Best Local Similarity 83.3
Matches 10; Conservative
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARX:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
PERATTER:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                             1 CFQWKRAMRKVR 12
                                                                                                                                                        2 CFOWORNMEKVR 13
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                            JS-07-891-174-3
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Gaps ö

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RESULT 9
US-08-256-711-25
| Sequence 25, Application US/08256771
| Patent No. 565631
| GANERAL INFORMATION |
| TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING |
| TITLE OF INVENTION: PRODUCTS THEREWITH |
| NUMBER OF SEQUENCES: 3
| ADDRESSEE; Wenderoth, Lind & Ponack |
| STREET: 805 Fifeenth Street, N.W., #700 |
| STREET: B0. Fifeenth Street, N.W., #700 |
| STREET: B0. Fifeenth Street, N.W., #700 |
| STREET: B0. COUNTRY: U.S.A. |
| COMPUTER READABLE FORM: Washington |
| STREET: B0. COMPUTER: ID COMPUTER READABLE FORM: WEDIUM TYPE: Diskette, 5.25 inch, 500 kb |
| COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPUTER: ID COMPU
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                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25:
                                                              85.5%;
83.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                              Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                  1 CFQWKRAMRKVR 12
                                                                                                                                                                                                                 2 CFOWORNMRKVR 13
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      US-08-256-771-24
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US-08-381-984-24
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Patent No. 565691

GENERAL INFORMATION:
APPLICANT: MAMORY TOMITA et al.
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
CITY: Washington
CITY: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Disketch, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: US.A.
APPLICATION NUMBER: US/08/256,771
FILING DATE: US/08/256,771
FILING DATE:
FILING DATE:
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Best Local Similarity 83.3%; Pred. No. 0.0016;
Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                        /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATMER WATER
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: DERI
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
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S-08-256-771-24
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RESULT 12
US-09-508-734-4

J GENERAL INFORMATION:

GENERAL INFORMATION:

A PAPLICANT: Samyang Genex Corporation

TILLE OF INVENTION:

TILLE OF INVENTION:

TILLE OF INVENTION: useful microorganism thereof

CURRENT APPLICATION UNMER: DC/00139

CURRENT FILING DATE: 1200-06-01

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1998-07-14

PRIOR FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
DENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | FRATURE:
| NAME/KEY:
| LOCATION:
| IDENTIFICATION METHOD:
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
| US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 0.0016;
1; Mismatches 1; Indels
                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 33,367
REGISTAATION NUMBER: 33,367
REGISTAATION NUMBER: 33,367
REGISTAATION NUMBER: 33,367
REGISTAATION NUMBER: TELECOMMUNICATION INPORMATION:
TELEBHONE: 202-371-8850
                STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25
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83.3%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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STRANDEDNESS: sin
                                                                   D.C.
                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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NAME/KST:
LOCATION:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thereo
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LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 85.5%; Score 59; DB 1; Length 20; Best Local Similarity 83.3%; Pred. No. 0.0016; Matches 10; Conservative 1; Mismatches 1; Indels
Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendercoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: BOS Fifteenth Street, N.W., #700
CITY: Washington
STREET: BOS FIFTEENTH N.W., #700
COUNTRY: U.S.A.
ZIP: 20005
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Disketre, 3.5 inch, 1.44 mb
COMPUTER READBLE FORM:
MEDIUM TYPE: Disketre, 3.5 inch, 1.44 mb
COMPUTER READBLE FORM:
MEDIUM TYPE: Disketre, 3.5 inch, 1.44 mb
COMPUTER READBLE FORM:
MEDIUM TYPE: Disketre, 3.5 inch, 1.44 mb
COMPUTER READBLE FORM:
APPLICATION NUMBER: US-008381,984
FILING DATE: APTORMATION:
APPLICATION NUMBER:
FILING DATE: ATTORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFONY:
TELEFONY: TELEFONY: 202-371-8850
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Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWKRAMRKVR 12
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US-08-381-984-25
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STRAIN:
STRAIN:
STRAIN:
STRAIN:
INDIVIDUAL ISOLATE:
DEVLOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
INMEDIATE SOURCE:
LIBRARY:
CHOOMOSONE/SEGMENT:
MAP POSITION:
WAP POSITION:
WAP POSITION:
WAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
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IDBNITICATION METHOD:
OTHER INFORMATION: (hote= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN N. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFA::
                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
SEQUEDICE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWKRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO A STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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3-09-508-734-6
5-09-508-734-6
5-09-508-734-6
5-09-508-734-6
5-09-508-734-6
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                                                                                                                                                                                                         85.5%; Score 59; DB 4; Length 22; 83.3%; Pred. No. 0.0018;
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S-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
CENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESSEE: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, Lind & Wenderoth, L
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Matches 10; Conservative
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
    LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
S-09-508-734-4
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ORGANISM: Homo sapiens
3-09-508-734-6
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Best Local Similarity
Matches 10; Conserv
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Search completed: February 21, 2003, 08:04:27
Job time : 9.93023 secs
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DOCUMENT NUMBER:
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VOLUME:
ISSUE:
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IDENTIFICATION METHOD:
OCHER INFORMATION: O'note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 21"
FRATURE:
NAME/KEY: modified site
LOCATION: 21
ESULT 15
IS-07-891-174-10
Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.

ZTATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Comparible

OPERATING SYSTEM: MS-DOS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,174

FLING DATE: 29-MAY-1992

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161

FILING DATE: 05-SEP-1991

ATPORNEY AGENT INPORMATION:

NAME: WATTEN M. Cheek UT.

REGISTRATION NUMBER: 33,367

REGISTRATION NUMBER: 33,367

REGISTRATION NUMBER: 33,367

REGISTRATION NUMBER: 33,367

REPERENCE/DOCKET NUMBER: 33,367

TELECOMMUNICATION INPORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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CELL TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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FRAGMENT TYPE;
ORIGINAL SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
MOLECULE TYPE:
HYPOTHETICAL:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cyg residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cyg residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 85.5%; Score 59; DB 1; Length 25; Best Local Similarity 83.3%; Pred. No. 0.002; Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
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us-09-743-107b-93.rapb

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Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 132, App
Sequence 131, App
Sequence 14, App
Sequence 16, App
Sequence 16, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 118, App
Sequence 166, App
Sequence 466, App
Sequence 416, App
Sequence 416, App
Sequence 418, App
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3 9 US-10-028-072-132

3 9 US-10-121-049-132

3 9 US-10-121-049-132

3 9 US-10-140-470-132

3 9 US-10-175-746-132

3 9 US-10-176-218-132

3 9 US-10-176-218-132

3 9 US-10-176-218-132

3 9 US-10-140-474-132

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6 US-09-986-582-46

7 US-09-986-582-46

7 US-09-986-582-6604

9 US-09-986-684-1346

9 US-09-974-864-1346

9 US-09-978-255A-466

9 US-09-978-122A-466

9 US-09-978-122A-466

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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: RALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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US-09-798-869-20
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Sequence 2, Appli
Sequence 42, Appl
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                                                                                      February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

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                    GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens; OTHER INFORMATION: sequence)
US-09-798-869-6
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Score 59; DB 9; Length 694;
Pred. No. 0.019;
1; Mismatches 1; Indels
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Pred. No. 0.01;
                                                   1; Indels
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Pred. No. 0.022;
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APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE FEPTIDES
FILE REFERENCE: AJ4049-FCT-USA-A
FILE REPERENCE: AJ4049-FCT-USA-A
FURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
FRIOR FILING DATE: 1999-08-31
FRIOR FILING DATE: 1599-08-31
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63.6%;
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Best Local Similarity 75.0%;
Matches 9; Conservative
  Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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                                                                                                       1 CFOWKRAMRKVR 12
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Best Local Similarity
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; ORGANISM: CAPRINE
US-09-798-869-3
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US-09-798-869-3
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; Sequence 2, Application US/10023096
; Patent No. U320020160941A1
GENERAL INFORMATION:
APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Tomasz
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES: Jacobson, Price, Holman & Stern.
STREET: 400 Seventh St. N.W.
COITY: Washington D.C.
TITLE OF LOWENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 9; I
Pred. No. 0.00078;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE OF INVENTION: BIOACTIVE PEPTIDES
TILLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-8
NUMBER OF SEQ ID NOS: 30
SOFWARE: FRANCE FILING DATE: 1998-08-8
SEQ ID NO 20
LENGTH: 25
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 83.3
Matches 10; Conservative
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US-09-798-869-20
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Pred. No. 1.2;
2; Mismatches
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOIN SIGNED SVENDSEN
APPLICANT: GYSTEN REKALL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND:
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A44049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: GB9818938-4
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                                                   US-00-798-869-4

Sequence 4, Application US/09798869

Publication No. US20030022821A1

GENERAL INPORMATION:
APPLICANT: JOHN SIGNED SYENDERN

APPLICANT: GENERN REMAL.
APPLICANT: APPLICANT: BALDUR SVEINBL(RNSSON)
APPLICANT: BALDUR SVEINBL(RNSSON)
APPLICANT: BALDUR SVEINBL(RNSSON)
APPLICANT: BALDUR SVEINBL(RNSSON)
TILLE REFERENCE: A34049-PCT-USA-A
CURRENT PILLOR DATE: 13001-02-27
PRIOR PILLOR DATE: 1999-08-31
PRIOR PLICATION NUMBER: GE9818938.4
PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE FEALESCO FOR Windows Version 4.0
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Best Local Similarity 54...
6; Conservative
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  1 CFOWKRAMRKV 11
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Best Local Similarity
Matches 6; Conserv
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ORGANISM: MURINE
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ORGANISM: MURINE
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llarity 54.5%; Pred. No. 0.49;
Conservative 3; Mismatches 2; Indels
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1; Indels
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Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: USTEIN SIGNEDSIN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OP INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESE for Windows Version 4.0
SEQ ID NO 7
LUNGTH: 15
Mismatches
                                                                                                                                                                                Sequence 23, Application US/09798869
Publication No. US20030022821A1
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: ALS USELAN
APPLICANT: BALDUR SVEINDS (RNSSON
APPLICANT: BALDUR SVEINDS (RNSSON
TITLE OF INVENTION: BIOACTUR PEPTIDES
TILE OF INVENTION: BIOACTUR PEPTIDES
CURRENT FILING DATE: 201-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTERQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
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ORGANISM: Artificial Sequence
7; Conservative
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Best Local Similarity
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                                                                                 3 CYCWORRMRKL 13
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                                        1 CFQWKRAMRKV 11
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Best Local Similarity
Matches 6; Conserv
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ORGANISM: CAPRINE
3-09-798-869-23
Matches
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1 CFQWKRAMRKV 11
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CRGANISM: BOVINE
US-09-798-869-29
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                                                                                                                                                       GENERAL INCOMETION:
APPLICANT: Feath, Sharron G.
APPLICANT: Feath, Sharron G.
APPLICANT: Feath, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Than Sharron G.
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APPLICANT: 
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OTHER INFORMATION: MAP TO AL096701.14
OTHER INFORMATION: EXPRESSED IN LUNG. SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HETA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXT HUMAN HIT: AM294800.1, EVALUE 1.00e-06
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                                                                         Sequence 47985, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION;
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ORGANISM: Homo sapiens
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S-09-864-761-47985
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RESULT 11

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RESULT 13 US-09-798-869-30

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Mduli, Khisimuzi Bekker, Linda-Gail Aphrea E.

"FLICANT: Bekker, Linda-Gail Applicant: The Government of the United States of America APPLICANT: The Government of the United States of America APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Matchdds of Diagnosing Multidrug Resistant Tuberculosis FILE REFERENCE: 015280-41310005
CURRENT APPLICATION NUMBER: US/09/888,320
CURRENT FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR PLING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 2
LENGTH: 489
TYPE: PPT
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ORGANIZM: Mycobacterium tuberculosis
OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
3-09-888-320-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 9; Length 15; Pred. No. 2.3;
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                                                 GENERAL INVORMATION.
GENERAL INVORMATION.
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,669
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 15
TYPE: PRICE PRICESO fOR WINDOWS VERSION 4.0
SEQ ID NO 30
LENGTH: 15
TYPE: PRICE
ORGANISM: BOVINE
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S-09-738-626-5715
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
Sequence 30, Application US/09798869
Publication No. US20030022821A1
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Best Local Similarity 54.5
Matches 6, Conservative
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Matches 5; Conserv
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Pred. No. 18;
5; Mismatches 1
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
LENGTH: 86
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                                                                                                                                                      APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                                                                                                                   / TYPE: PRT
/ ORGANISM: Corynebacterium glutamicum
US-09-738-626-5715
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            IZOGUCHI, HIROSHI
                                             HAYASHI, MIKIRO
OCHAAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
NAKAGAWA, SATOSHI
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Best Local Similarity 45.5
Matches 5; Conservative
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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rfect score:
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## ALIGNMENTS

RESULT 1 ITEMU acctransferrin precursor [validated] - human Nationare names a accoderin Incortansferrin precursor [validated] - human Nationare names a accoderin Incortansferrin precursor [validated] - human (Species Homes and accoderin Incortansferrin precursor [validated] - human (Species Homes and accoderin Incortante names and accoderin Incortante names and accoderin Incortante and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies and accompanies accompanies accompanies and accompanies and accompanies accompanies accompanies accompanies and accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompanies accompani
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lactoferrin - sheep (fragment)

(species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

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(spaces)

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R,Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
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A;Experimental source: clone F53H4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
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A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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65.2%; Score 45; DB 2; Length 275;
Best Local Similarity 72.7%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                  Length 708,
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54.5%; Pred. No. 0.15;
iive 4; Mismatches
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Pred. No. 0.79;
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Whendo, T.A.; Wei, X.; Benz Jr., E.J.

Slood 70, 989-993, 1987

Fittle: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR procession: S07160; MUID:88001031; PMID:3477300

Whence number: S07160; MUID:88001031; PMID:3477300

Whence the type: mRNA

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Victors references: GDB:119368; OMIM:150210
Viking position: 3q21-3q23
Visuperfamily: transferrin; transferrin repeat homology
Vikeywords: duplication; glycoprotein; iron binding; milk
Vill-19/Domain: signal sequence #status predicted <SIG>
Vill-19/Domain: signal sequence #status predicted <SIG>
Vill-19/Domain: transferrin repeat homology <TRHI>
Vill-366/Domain: transferrin repeat homology <TRHI>
Vill-368/Domain: transferrin repeat homology <TRHI>
Vill-368/Domain: transferrin repeat homology <TRHI>
Vill-369/Domain: transferrin repeat homology <TRHI>
Vill-360-699/Domain: transferr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ); Residues: 3-701, 'SWKEVN' < PAN>
); Experimental source: normal breast tissue
}; Metz-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Jur. J. Biochem. 145, 659-666, 1994
); Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
); Reference number: A31000; MUID: 85076667; PMID: 6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assignment of the relevant locus
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'Residues: 20-140.142-169.171-203,'L'.205,'K',207-208,'K',210-385,'Q',387-391,'W',393-
'Residues: 20-140.142-169.171-203,'L'.205,'K',207-208,'K',210-385,'Q',387-391,'W',393-
'Note: the final paper in a series
'Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

Nur. J. Biochem. 241, 303-308, 1996
'NTILE: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affiliation: S74119; MUID:97054624; PMID:8898921
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\(\text{Residues: 1-708 clsP>}\)
\(\text{Sesidues: 1-708 clsP>}\)
\(\text{Superfamily: transferrin repeat homology}\)
\(\text{Seywords: duplication; glycoprotein}\)
\(\text{359-696/bomain: transferrin repeat homology <\TRH2>}\)
\(\text{359-696/bomain: transferrin repeat homology <\TRH2>}\)
\(\text{359-696/bomain: transferrin repeat homology claus)}\)
\(\text{(covalent) #status predicted}\)
\(\text{359-696/bomain: transferrin repeat homology claused)}\)
\(\text{(covalent) #status predicted}\)
\(\text{(covalent) #status predic
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Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
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;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Siochem Biophye, Res. Commun. 203, 1324-1332, 1994
;Title: Characterization of the goat lactoferin CDNA:
i;Reference number: JC2323; MJID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atus; not compared with conceptual translation
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Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
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Length 208; Indels

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C;Superfamily: phytochrome, phytochrome homology Kskywordes chromoprotein, dimen; photochromoprotein, dimen; photoceceptor; phytochromoprotein, phytochrome homology <PHX> F;65-581/Domain: phytochrome homology <PHX> F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Sorghum bicolor (sorghum)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Accession: T14803
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Pratt, L.H.; Morgan, P.W.; Mullet, submitted to the EMBL Data Library, April 1996
A;Reference number: Z18186
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45.5%; Pred. No. 22;
ive 4; Mismatches 2; Indels
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A;Molecule type: mRNA
A;Residues: 1-1135 <CHI>A;Residues: 1-1135 <CHI>CGTOS: Teferences: EMBL:U56731; NID:g1800218; FID:g1800219
C;Genetics:
                                                                                                                                                                                                                           Score 43; DB 2;
Pred. No. 2.9;
1; Mismatches
            A, Experimental source: strain 16M
C, Genetics:
A, Gene: BME115.1
A, Map position: 1
C, Superfamily: pyridoxamine-phosphate oxidase
C, Keywords: oxidoreductase
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ilarity 58.3%;
Conservative 1
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Matches 5; Conservative
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Best Local Similarity
Matches 7; Conserv
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A; Gene: CESP: F09C3.1
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Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.

Sage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell

KATP, P.; Romero, P.; Zhang, S.

Haring, P.; Romero, P.; Zhang, S.

Hathors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
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Date: il-Jan_2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
1.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Litle: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       er, B.W.
Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens CS8.
Reference ninger: AB2577; PMID:11743193
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Experimental source: strain CS8 (Dupont)
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Molecule type: DNA
Residues: 1-208 «KUR»
Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
                                                                                                                                                                                                                                                 Cross-references: GB: AE007869; PIDN: AAK86569.1; PID: 915155733; GSPDB: GN00169
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Pred. No. 2.9;
1; Mismatches 4; Indels
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58.3%; Pred. No. 2.9;
iive 1; Mismatches
                                                                                                                                                                                                                                                                                                    Gene: AGR C 1381
Map position: circular chromosome
Superfamily: pyridoxamine-phosphate oxidase
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Map position: circular chromosome
Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 58.3%;
Matches 7; Conservative
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1es 7; Conservative
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Molecule type: DNA
Residues: 1-206 <KUR>
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A;Introns: 53/2; 134/3; 283/1; 662/1; 731/3; 787/1; 976/3; 1043/2; 1171/3; 1267/2; 1354/?
                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-1391 <WIL>
A;Cross-references: EMBL:292781; PIDN:CAB07179.2; GSPDB:GN00019; CESP:F09C3.1
A;Experimental source: clone F09C3
Appointational protein F09C3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: La-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20642
R;Lennard, N.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19304
A;Reference number: Z19304
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A;Molecule type: DNA
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32K protein - vaccinia virus (strain WR) (fragment)
C;Species: vaccinia virus
C;Species: vaccinia virus
C;Species: vaccinia virus
C;Date: 25-dul-1991 #sequence_revision 26-Jul-1991 #text_change 21-Jul-2000
C;Accession: A36415
R;Pacha, R.F.; Meis, R.J.; Condit, R.C.
A;Title: Structure and expression of the vaccinia virus gene which prevents virus-induces A;Reference number: A36415; MUID:90317884; PMID:2370683
                                                                                                                                                                                                                                                                                                                                                                                           A; Cross_references: EMBL: Z48758; NID: 9747879; PIDN: CAA88678.1; PID: 9747899; MIPS: YDR125c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
A. Cell Sci. 107, 635-644, 1994
A;Fitle: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes. A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
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N.Alternate names: Wypotherical protein YD9727.20c
C.Species: Saccharomyces cerevisiae)
C.Species: Saccharomyces cerevisian protein YD9727.20c
C.Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 24-Sep-1999
C.Accession: 55260
R.Murphy, L., Shore, L., Harris, D.
submitted to the EMBL Data Library, March 1995
A.Accession: 55260
A.Molecule type: DNA
A.Molecule type: DNA
A.Accession: 1453 AUR>
A.Accession: 1453 AUR>
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C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-456 <MIT>
A;Cross.reference: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
A;Experimental source: strain 21gr
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56.5%; Score 39; DB 2; Length 456
Best Local Similarity 41.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 3; Indels
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C; Keywords: nuclectide binding; P-loop
P;1919-1926/Region: nuclectide-binding motif A (P-loop)
F;2202-22209/Region: nuclectide-binding motif A (P-loop)
F;2530-2537/Region: nuclectide-binding motif A (P-loop)
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A,Cross-references: SGD:S0002532; MIPS:YDR125c
A,Map position: 4R
C,Superfamily: hypothetical protein YDR125c
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                                                                                                                                                                                                                                                                               Accession: B87998
janonymous, The C. elegans Sequencing Consortium.
janonymous, The C. elegans Sequencing Consortium.
janonymous, The C. elegans Sequence of the nematode C. elegans: a platform for investigating biolog; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog; Reference number: A75000; MUID:99069613; PMID:9851916
j.Note: see websites genome.wnstl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and shocession: B87998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
;Molecule type: DNA
;Residues: 1-1397 <STO>
;Cross references: GB:chr_I; PIDN:CAB07179.1; PID:g3875638; GSPDB:GN00019; CESP:F09C3.1
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'Species: Mus musculus (house mouse)
'Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
'Accession: A28438', A41205
'Penteccst, B.T.; Teng, C.T.
Biol. Chem. 262, 10134-10139, 1987
'Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre', Reference number: A92596; MUID:87280033; PMID:3611056
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, Residues 3-70 × PEBN-
, Crose-references: EMBL:J03298
:;Liu, Y.; Teng, C.T.
E Biol. Chem. 266, 21880-21885, 1991
, Title: Characterization of estrogen-responsive mouse lactoferrin promoter., Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                   rotein F09C3.1 [imported] - Caenorhabditis elegans
Species: Caenorhabditis elegans
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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V.Residues: 1-15 <LIU>
V.Cross-references: GB:N74778
V.Superfamily: transferrin; transferrin repeat homology
V.Superfamily: transferrin; transferrin predicted <SIG>
V.1-19/Domain: signal sequence #status predicted <SIG>
V.20-707/Product: lactorransferrin #status predicted <MAT>
V.358-695/Domain: transferrin repeat homology <TRH2>
V.494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 32;
2; Mismatches 3; Indels
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Pred. No. 40;
1; Mismatches
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59.4%;

Conservative

Query Match Best Local Similarity Matches 7; Conserv

Map position: 1 Gene: F09C3.1

Genetics:

122 ÓWRRAMESVR 131

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3 QWKRAMRKVR

actoferrin precursor - mouse

ESULT 11

Accession: A28438

Accession: A41205

Query Match 58.0%; Best Local Similarity 54.5%; Matches 6; Conservative ;

CFOWKRAMRKV 11 37 CLRWONEMRKV 47

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ESULT 12

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Status: preliminary
Molecule type: DAA
Residus: 1-275 <PAC>
Cross-references: EMBL:M32064; NID:g335834; PIDN:AAA48348.2; PID:g755535
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0; Gaps ; 0 Ouery Match 55.1%; Score 38; DB 2; Length 275; Best Local Similarity 60.0%; Pred. No. 29; Matches 6; Conservative 1; Mismatches 3; Indels

1 CFQWKRAMRK 10

185 CLEWLRAKRK 194

potherical protein A17L - variola major virus
Species: variola major virus
Species: variola major virus
Species: variola major virus
Species: variola major virus
Accession: T2858
Massung, R. F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Tile: Species of variola virulence determinants in terminal regions of variola smallpox virus
Reference number: Z20488; MUID:94088747; PMID:8264798
Accession: T2858
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 11377 cMAS>
Cross-references: EMBL:L22579; NID:9623595; PIDN:AAA60868.1; PID:9439038
Experimental source: strain Bangladesh-1975

Gaps . 0 Score 38; DB 2; Length 377; Pred. No. 40; 1; Mismatches 3; Indels Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative

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185 CLEWLRAKRK 194

arch completed: February 21, 2003, 08:02:48
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hesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
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TISSUE-Mammary gland;
MEDILINE-90364839; PubMed=2402455;
REY M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                              21-UU-1986 (Rel. 01, Created).
15-UU-1999 (Rel. 38, Last sequence update)
15-UN-2002 (Rel. 41, Last amnotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin .
Lactoferroxin B; Lactoferroxin C).
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-Mammary gland;
Liang Q., Jimenez-Plores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.",
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUTENCE FROM N.A.
TISSUE=Bone marrow;
TISSUE=Bone marrow;
"Human neutrophil lactoferrin coding and 5' flanking region DNA"
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P02788; Q16780; Q16785; Q16789; Q00756; Q9H1Z3; Q96KZ4;
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TISSUE-Mammary gland;
TOSOME-Mammary gland;
"Cheng H., Chen X., Huan L.;
"CDNA Cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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7LES_DROME
SYB2_RHIME
CCHL_CCNAL_
NOV_CHICK
GLGA_BACST
NCAP_LYCVA
NCAP_LYCVA
NOAP_LYCVA
ENV_HY2CR
PHY1_CREPU
PHY1_CREPU
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TISSUE-Prostate;
Strausberg R.;
Submitted (OCT-2001) to
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TISSUE=Mammary gland;
Cho Y.Y.;
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PHYC_ORYSA
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OF 3-711 FROM N.A.

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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell B., Solinsky K.A., Desilva U., Diagranti J.L., Sagripanti J.L., Sagripanti J.L., Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=2585506;
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"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
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"The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haridas M., Anderson B.F., Baker B.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An 88 amino acid long C-terminal sequence of human
                        Powell M.J., Ogden J.E.;
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MEDLINE=97156796; PubMed=9003186;
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MEDLINE=99190892; PubMed=10089347;
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MEDLINE=90326549; PubMed=2374734;
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MEDLINE=82262043; PubMed=7049727;
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-1- FUNCTION: TRANSPERRING BARE IRON BINDING TRANSPORT PROTEINS WHICH

-2AN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.

-1- FUNCTION: LACTOPERROXINS A, B AND C HAVE OPICID ANTAGONIST

LACTOPERROXIN A SHOWS PREPERENCE FOR MU-RECEPTORS, WHILE

LACTOPERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS. CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE-91166929; PubMed=1369293;
Tani F., Ilo K., China H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived" Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus Klittworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanal A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
Butri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.; Teng C.T.; Teng C.T.;
Familial subepithalial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998) Jameson G.B., Anderson B.F., Noris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; -i- SUBCELLUTAR LOCATION: Secreted.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY. K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS). from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990) Acta Crystallogr. D 55:403-407(1999). MEDLINE=99192677; PubMed=10089508; AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -. EMBL, X53961, CAA37914.1, -. EMBL, U07643, AAB60324.1; -. EMBL, M93150, AAA36159.1; -. AAB57795.1; -. M83205; AAA58656.1; -. M18642; AAA86665.1; -. M83202; AAA59511.1; -. VARIANTS THR-30 AND ARG-48. M73700; AAA59479.1; X52941; CAA37116.1; 12-MAR-97. 21-APR-97. 1LCF; 31-AUG-94. 1LCT; 31-OCT-93. 1LFG; 31-JUL-94. 1LFH; 31-OCT-93 1LFI; 31-OCT-93 31-AUG-94 1LGB; 31-AUG-94 08-MAR-96 SUBUNIT: MONOMER 1BKA; EMBL; PDB; PDB; PDB; PDB; PDB; PDB; PDB; PDB; 

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=94380047; PubMed=8093048;

MEDLINE=94380047; PubMed=8093048;

Le Provost F., Nocart M., Guerin G., Martin P.;

Le Provost F., Nocart M., Guerin G., Martin P.;

Electrization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine Ul2 syntemy group.";

Biochem. Blophys. Res. Commun. 203:1324-1332(1994).

-i - FUNCTION: TRANSFERRINS ARE LOON BINDING TRANSPORT PROFIEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

-i - SUBUNIT: NONOMER (BY SIMILARITY).

-i - SUBCINITAL LOCATION: Secreted.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
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STRAIN-Somali; TISSUB=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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InterPro; IPR01156; Transferrin.
Pfan; PF00402; transferrin; 2.
PRIWTS; PR00402; TRANSFERRIN; 2.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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09TUMO; 09MZS5;
16-0CT-2001 (Rel. 40, Last seq.
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                                                                                                                                                                                                                                              InterPro; 1PR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SNART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN_2; 2.
PROSITE; PS00206; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_2; 2.
PROSITE; PS00207; TRANSFERRIN_3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal.

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Pred. No. 0.19;
3; Mismatches 1; Indels
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Q -> K (IN REF. 2).
P -> P (IN REF. 2).
F -> P (IN REF. 2).
S -> R (IN REF. 2).
D -> G (IN REF. 2).
F2EDA3C83539960D CRC64;
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DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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708 AA;
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MEDLINE=97198556; PubMed=9046599;

MEDLINE=97198556; PubMed=9046599;

Childs K.L., Miller P.R., Cordonnier-Pratt M.-M., Pratt L.H.,

Anorgan P.W., Millet J.E.;

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

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"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytochrome B.";

"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a phytoperiod sensitivity g
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                                                                                                                                                                      Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBUNIT: HOMODIMER (BY SIMILARITY).
-:- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
-:- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
-:- SIMILARITY: CONTAINS 2 PAS (FER-ART-SIM) DIMERIZATION DOMAINS.
-:- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (FAC) DOMAIN.
-:- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                   (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
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InterPro; IPR0015594; AIPbind_ATPase.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR001661; PAG.
InterPro; IPR001610; PAG.
InterPro; IPR001014; PAG.
InterPro; IPR001294; PAYFOOHrome.
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Pfam; PF00512; asignal; 1.
Pfam; PF00599; PAS; 2.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase c; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM0065; GAF; 1.
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SMART; SM00388; HisKA; I.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
STANDARD;
                                                                                                                                          Phytochrome C.
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HSSP, P02788; ICB6.
MGD; MG196837; Ltf.
InterPro; IPR001156; Transferrin.
PFRUNCS; PR00402; TRANSFERRIN.
PRINCS; PR00402; TRANSFERRIN.
PROSITE; P800205; TRANSFERRIN.
PROSITE; P800205; TRANSFERRIN.
PROSITE; P800207; TRANSFERRIN.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11arity 54.5%; Score 40; DB 1; Length 707; Conservative 2; Mismatches 3; Indels
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EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
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Q9ZWI9; P93429;
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16-OCT-2001 (Rel
15-JUN-2002 (Rel
Phytochrome C.
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DT 16-OCT-
DT 15-UCT-
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MEDLINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885 (1951).

-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-LANGTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ACOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-! SUBUNIT: MONOMER.
-! SUBCLIULIAR LOCATION: Secreted.
-! DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-! SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
PROSITE; PS00245; PHYTOCHROME 1; FALSE_NEG.
PROSITE; PS50046; PHYTOCHROME 2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
PAS 1.
DOMAIN 748 832 PAS 1.
DOMAIN 902 1122 PAS 2.
BINDING 321 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-87280033; PubMed-3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                          DB 1; Length 1135;
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TISSUE-Uterus;
Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P08071; P70690; Q61799; Q922P2; U1-AUC-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                         Score 42; DB 1
Pred. No. 6.2;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            707 AA
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J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                         60.9%;
45.5%;
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Best Local Similarity
Matches 5; Conserv
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FL_MOUSE
TRFL_MOUSE
P08071; P70
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Oryza sativa (Rice). Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.

NCBI_TaxID=4530;

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[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Takano M.;
Tahir M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of "Thytochrome C (PHYC) gene in rice: isolation and characterization of "Thytochrome C (PHYC) gene in rice: isolation and characterization of "Thytochrome C (PHYC) is sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 275-378 FROM N.A. MEDILINE=97019052; PubMed=886568; MATHEWS S., Sharrock R.A.; "The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00245; PHYTOCHROME_1; 1.
PROSITE; PS50045; PHYTOCHROME_2; 1.
Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
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Pfam; PF02518; HATPASS C; 1.
PRINTS; PR01033; PHATPASS C; 1.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASS C; 1.
SMART; SM00389; HisKa; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRRAMS; TIGRROL29; SENSOTY_box; 2.
PROSITE; PS50102; HIS KIN; 1.
PROSITE; PS50112; PAS; 2.
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Interpro; IPR003169; GAF.
Interpro; IPR001661; His_KIN sig.
Interpro; IPR001661; His_Kin Sig.
Interpro; IPR001601; PAC.
Interpro; IPR00114; PAC.
Interpro; IPR00114; PAC.
Interpro; IPR001294; Phytochrome.
Ffam; PF00806; phytochrome; 1.
Ffam; PF008012; signal; 1.
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EMBL; U61207; AAB41996.1; -.
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STRUEBERFREIN, N. S. STRUEBERFREIN, N. STRUEBERFREIN, N. STRUEBERFREIN, N. STRUEBERFREIN, N. STRUEBERFREIN, S. ABBURDER M., HOOKING R.A., Galle R.F., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gacayne J.D., Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N., Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Barach R.G., Champe M., Pfeiffer B.D., Raman R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Ram K.H., Doyle C., Baxerer E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A. An H.-J., Andrews Pfannkoch C., Badarin D., Rallev R.W., Baran B.P., Bhandari D., Botcharvo S., Barnan B.P., Bhandari D., Botcharvo S., Botchan W.R., Boutck J., Brokstein F., Brottier P., Borkova D., Botchan M.R., Boutck J., Brokstein P., Brottier P., Borkova D., Dew I., Davis S., Dahlke C., Pavandari P., Brottier P., Bornes B.W., Bandley S., Dahlke C., Pavandari B., Davis S., Dubon R.C., Botchan M., B., Davis S., Dubon R.C., Botchan M., B., Davis S., Dubon R.C., Pavander S., Fleischmann W., Rodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Botchin D., Houston K.A., Heiman T.J., Hermandez J.R., Houck J., Hock M., Gabriellan M.E., Garral J.H., Gu Z., Guan P., Harris M., Adarsey D., Lai S., Marye A.J., Heiman T.J., Hermandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z., Liang Y., Lin X., Marteil B., McIncosh T.C., Mczwitz S., Kunison J.A., McCatell J., Muzny L., Muzny D.M., Neber D.C., Scheler F., Schadting A.C., Standers R., Paller R., Samth T., Ra Reinert K., Remington M., Stupski M., Pikmer B., Muzny D., M., Stupski M.P., Smith T., Ra Shies R., Tector C., Tunner R., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weinstock
                                                                                                                                                                                          Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapo
Insecta, Pterrygota, Neoptera, Endopterrygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                            ..
0
                                                                                                                                                 Score 40, DB 1; Length 1137;
Pred. No. 15;
3; Mismatches 3; Indels
                                   HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY)
F -> S (IN REF. 2).
C -> S (IN REF. 2).
                                                                                                                F2A520181CFE7B32 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                         Q9XZL8; Q9V391;
30-7XY-2000 (Rel. 39, Created)
30-7XY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           292 AA
PAS 1.
PAS 2.
                                                                                                                  125982 MW;
                                                                                                                                                       58.0%;
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690
824
1124
322
279
620 690
750 82,
904 112,
322 32;
279 27,
292 292
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nebula protein.
NLA OR CG6072.
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DOMAIN
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BINDING
CONFLICT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Smith H.(Glibbs R.H., Myers E.W., Rubin G.W., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195(2000).
-!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
-!- FUNCTION: THE DELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALPHA, BETA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocalee;
Chlamydomonadaceae; Chlamydomonas.
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InterPro; IPR004273; Dynein_heavy.
Pfam; PP03028; Dynein_heavy; 1.
Colled coil.
Arctingues; Dynein; ATP-binding; Flagella; Donain.
Colled coil.
Colled coil.
                                                                                                                                                                                                                                                                                                                                                                                    Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64FlBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 39; DB 1;
54.5%; Pred. No. 5.3;
iive 3; Mismatches
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAV-2000 (Rel. 39, Last annotation updat
Dynein beta chain, flagellar outer arm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                            EMBL; AF147700; AAD33987.1; -. EMBL; AE003712; AAF55285.1; -.
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Matches 6; Conserv
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SEQUENCE FROM N.A.
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01-NOV-1997 (
30-MAY-2000 (
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                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPOEC operon.";
Submitted (May.1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CAPALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Planet P., Jagoueix S., Bove J.M., Garnier M.; "Detection and characterization of the African Citrus Greening Liberobacter by amplification, cloning and sequencing of the rplKAJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
1175 COILED COIL (POTENTIAL).
1400 COILED COIL (POTENTIAL).
1825 COILED COIL (POTENTIAL).
1826 COILED COIL (POTENTIAL).
2045 MICROTUBLE-BINDING (POTENTIAL).
3128 COILED COIL (POTENTIAL).
3425 COILED COIL (POTENTIAL).
3426 COILED COIL (POTENTIAL).
3728 COILED COIL (POTENTIAL).
3728 ATP (POTENTIAL).
2509 ATP (POTENTIAL).
2537 ATP (POTENTIAL).
2538 ATP (POTENTIAL).
359961 MM; 9A9AS393C7C36AE7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
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InterPro; IPR001572; RNA_pol_B.

PROSITE; PS01166; RNA_Pol_BETA; PARTIAL.

Transferase; Transcription; DNA-directed RNA polymerase.

NON_TER 146 146

SEQUENCE 146 AA; 16731 MW; 815D6EDD66FDR943 CRCK4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                              11650
20455
33485
33485
33425
11926
22509
25537
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2530 253
2879 286
4568 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWKRAMRKVR 12
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Virology 179:247-266(1990)
              [2]
COMPLETE GENOME
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005962;
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TLCE_RICPR
                                                                                                                                                                                                                                                                                                                                              Matches
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              Gaps
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=90317884; PubMed=2370683;
Pacha R.F., Meis R.J., Condit R.C.;
Structure and expression of the vaccinia virus gene which prevents virus-induced breakdown of RNA.";
J. Virol. 64:3853-3863(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al6L.
Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                       A16L.
Vaccinia virus (strain WR).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
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MEDINE=91021027; PubMed=2219722;
GGODEL S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.;
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              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AA; 31811 MW; E2461AB1DB7B93A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY
                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete DNA sequence of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 17, Created)
(Rel. 17, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                       275 AA
 Pred. No. 3.9;
0; Mismatches
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. $0.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
              6; Conservative
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                                                                                                                                       STANDARD;
                                                                                                                                                                              01-AUG-1990 (Rel. 15, Le
16-OCT-2001 (Rel. 40, Le
Protein A16 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 CLEWLRAKRK 194
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Best Local Similarity
Matches 6; Conserv
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  Best Local Similarity
                                          1 CFQWKRAMRK 10
                                                                   10 CVQWSRGARK 19
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NCBI_TaxID=10254;
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NCBI_TaxID=10249;
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01-FEB-1991 (
16-OCT-2001 (
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                                                                                                                                      VA16_VACCV
P16710;
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A16_VACCC
D _VA16_VAC
C P20993;
              Matches
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BIEDLINE=299139499; PubMed=9823893;

Andersson S.G.B., Zomorodipour A., Andersson J.O.,

Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,

Briksson A.-S., Winkler H.H., Kurland C.G.;

"The genome sequence of Rickettsia prowazekii and the origin of mitochondria."
Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
Paoletti E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                        "Appendix to 'The complete DNA sequence of vaccinia virus'.";
'Nirology 179:517-563(1990).
-!- SIMILARITY: BELONGS TO THE POXVIRUSES A16 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.1%; Score 38; DB 1; Length 378; 60.0%; Pred. No. 11; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43561 MW; OSED614AA1D11A19 CRC64;
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16-0CT-2001 (Rel. 40, Last annotation update)
ADP,ATP carrier protein 5 (ADP/ATP translocase 5).
TLCS OR TLCS OR RP739.
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Interpro; IPR0042519.
Pfam; PF03003; DUF230.
SEQUENCE 378 AA; 43561 MW;
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                                                                                                                                         EMBL; Y11778; CAA72457.1; -.
InterPro; IPR004667; ADP_ATP_car.
Pfam; PF03219; TLC; 1..
TIGREAMS; TIGR00769; AAA; 1.
TIGREAMS; TIGR00769; AAA; 1.
Transmembrane; Transport; ATP-binding; Multigene family;
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Gaps ; 0 Length 500; 3; Indels ï Score 38; DB 1 Pred. No. 14; 2; Mismatches 55.1%; Query Match
Best Local Similarity 54.5
Matches 6; Conservative

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|| | |:||: 482 CFAWIYAVRKI 492 1 CFQWKRAMRKV 11

856 AA PRT; STANDARD; ENV HV2NZ P05883;

01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein G9160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

(isolate NIH-Z) (HIV-2) Human immunodeficiency virus type 2 (isolate NIH-Z) Viruses; Retroid viruses; Retroviridae; Lentivirus.

NCBI_TaxID=11719;

SEQUENCE FROM N.A.
MEDLINE-88320359; PubMed=3261862;
Zagury J.F., Franchini G., Reitz M.S. Jr., Collalti E., Starcich B.R., Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laure F., Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C., "Genetic variability between isolates of human immunodeficiency virus (HIV) type 2 is comparable to the variability among HIV type 1."; Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

HIV; J03654; ENV\$2NIHZ. InterPro; IPR000328; Env GP41. InterPro; IRR000777; GP120. Pfam; PF00516; GP120; 1. Pfam; PF00517; GP41; 1. AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; EMBL; J03654; AAB00761.1; -

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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Sevenless protein (EC 2.7.1.112). PRT; 2594 AA STANDARD; LES DROVI P20806; 7LES I 

Drosophila virilis (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Bukaryota; Metazoa; Arthropoda; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7244; MEDLINE=90319110; PubMed=2115169; Michael W.M., Bowtell D.D.L., Rubin G.M.; "Comparison of the sevenless genes of Drosophila virilis and Drosophila melanogaster. SEQUENCE FROM N.A.

tyrosine phosphate. Proc. Natl. Acad. Sci. U.S.A. 87:5351-5353(1990).

-!- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO

-!- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO

INSTRUCT A CELL TO DIFFERENTIATE INTO A R7 PHOTORECEPTOR. THE

LIGAND FOR SEV I THE BOSS (BRIDE OF SEVENLESS) PROTEIN.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

RECEPTOR SUBFAMILY.
-!- SIMILARITY: CONTAINS 7 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- CAUTION: UNCLEAR WHETHER THE POTENTIAL MEMBRANE SPANNING REGION NEAR THE N-TERMING IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE

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                                                                                                                                                                                   EMBL; M34545; AAA28883.1; -.

R EMBL; M34544; AAA28883.1; JOINED.

R EMS.; M35774; A35774.

R HSSP; P11362; 1FGK.

R InterPro; IPR000139; EMk pkinase.

R InterPro; IPR000139; EMk pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00069; pkinase; 1.

R Pfam; PR001061; Euk pkinase; 1.

R SMART; SM00135; LY; 1.

R SMART; SM00135; LY; 1.

R SMART; SM00135; LY; 1.

R ROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00107; PROTEIN KINASE DOM; 1.

R R ROSITE; PS00107; PROTEIN KINASE DOM; 1.

R R ROSITE; PS00107; PROTEIN KINASE DOM; 1.

R R ROSITE; PS00107; PROTEIN KINASE DOM; 1.
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77D8A356CBAD0BBD CRC64;
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FIBRONECTIN TYPE-III 6.
FIBRONECTIN TYPE-III 6.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1011—TaxID=3702;
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R MELL' 108315; AAA17742.1; ...
R InterPro; IFR001580; Calreticulin.
R PEAN, PR00626; Calreticulin; 1.
R PRINTS; PR00626; Calreticulin; 1.
R PROSITE; PS00803; CALRETICULIN. 1.
R ROSITE; PS00804; CALRETICULIN. 2; 1.
R ROSITE; PS00805; CALRETICULIN. 2; 1.
R ROPEST; Chaptrone.
T CALLIN. 26 S28 CALREXIN HOMOLOG 2.
T CHAIN 26 S28 CALREXIN HOMOLOG 2.
T TRANSMEM 467 POTENTIAL.
T DOMAIN 488 528 CYTOPLAGNIC (POTENTIAL).
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T REPEAT 27 238 1-1.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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Score 38; DB 1; Length 2594;
Pred. No. 81;
4; Mismatches 2; Indels
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STRAIN=CV. COlumbia;
BOYCe J., Coates D., Evans D.;
"Genomic sequence of a calnexin homologue from Arabidopsis
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SEQUENCE 528 AA; 60017 MW; C888DA1391B651EE CRC64;

0; Gaps Query Match Best Local Similarity 50.0%; Pred. No. 23; Matches 5; Conservative 3; Mismatches 2; Indels

0

1 CFQWKRAMRK 10 | :||| | :: 315 CGEWKRPMKR 324

arch completed: February 21, 2003, 07:51:40 b time : 6.2093 secs

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Q8vwm1 triticum ae Q6fvwm1 triticum ae Q6f16 homo saplen P88213 human immun Q98815 human immun Q8f213 accharonyc Q8unf5 human immun Q91699 human immun Q97855 human immun Q97855 human immun Q98m12 cicer ariet Q8am2 homo saplen Q85389 variola maj Q87209 camelpox viru Q91162 voriola wir Q87182 human immun Q98m12 variola maj Q87209 camelpox viru Q91182 homo saplen Q94213 human immun Q98761 cicer ariet Q85389 variola maj Q87209 camelpox viru Q91182 homo saplen Q94613 human immun Q98761 cicer ariet Q86313 human immun Q98761 human immun Q98761 human immun Q98761 human immun Q98761 human immun Q98851000 Q65882 encephalito
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
Homo saplens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2010 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC2247; AAH2347.1; -
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 AA
Q9M7A9
Q9GNW1
Q9GNW1
Q9BBH5
Q6BS213
Q6BSE2
Q00054
Q000623
Q9UNF5
Q910699
Q910823
Q95ML1
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Best Local Similarity 81.8%;
Matches 9; Conservative
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TISSUE=PROSTATE;
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Q9ucy5 homo sapien
Q9tr80 ovis aries
Q93780 caenorhabdi
Q86a0 rhizobium 1
Q8uc2 agrobacteri
Q9xr8 rhizobium m
Q8yfk3 brucella me
Q8yfk3 brucella me
Q9xf8 lycopersico
Q1118 human immun
Q9xf6 ovyza sativ
O9x65 ovyza sativ
O9x65 human ind
Q9xf1 hemo sapien
Q94517 homo sapien
Q94517 homo sapien
                                                                                                                                        February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                  GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                            tal number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         st-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       protein - protein search, using sw model
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Q9UCY5
Q9T00
Q91780
Q91780
Q91780
Q92RH8
Q8YFK3
Q92RH8
Q17772
Q92RP5
Q92RP5
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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sult No.

Length 275;

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"Genome sequence of the nematode C.elegans: A platform for
                                                           investigating biology.";
Science 282:2012-2018 | ...
EMBL; Z81099; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
              MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                 Local Similarity 72.7
Les 8; Conservative
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les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesorhizobium loti.";
DNA Res. 7:331-338(2000)
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                                                                                                                                                                                                              262 FOWKISMRKTR 272
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SEQUENCE 205 AA:
 SEQUENCE FROM N.A.
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Q986A0;
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Matches
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08 UHCZ
AC 08 UHCAC
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DE PYZIC
GN PDXH
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Q986A0
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 19, Last annotation update)
F53H4.4 protein.
F53H4.4. Caenorhabditis elegans.
Caenorhabditis elegans.
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL TAXID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                        Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TEBMBLEE]. 13, Last sequence update)
01-UNA-2000 (TEBMBLEE]. 13, Last sequence update)
01-UNA-2000 (TEBMBLEE]. 17, Last annotation update)
Lactoferrin (Fregment).
Ovis aries (Sheep).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, CaplaxID=9940;
                                                                                                                                                                                                                                          ;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                           Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 6; Length 33;
Pred. No. 0.26;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
[2]
                                                                                                Beminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; PO2788; IBKA.
InterPro; IPRO01156; Transferrin.
Pfam; PF00405; transferrin; 1.
SFOUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95127729; PubMed=7827104; MEDLINE=95127729; PubMed=7827104; Qian Z.Y. Jolles P., Migliore-Samour D., Fiat A.M.; Qian Z.Y. Jolles P., Migliore-Samour D., Fiat A.M.; HSCP; O77698; 1CE2.
InterPro; IPRO01156; Transferrin.
ERGÜTENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                          72.5%; Score 50; DB 4;
81.8%; Pred. No. 0.058;
tive 1; Mismatches
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                                           SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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54.5%;
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01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 54.2
Les Local 6; Conservative
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Best Local Similarity
Matches 9; Conserv
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9TR80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-JUN-2002 (TrEMBLiel. 21, Last sequence update)
01-JUN-2002 (TrEMBLiel. 21, Last sequence update)
01-JUN-2002 (TrEMBLiel. 21, Last annotation update)
Pyridoxamine 5'-phosphate oxidase.
PyXHOKOAMINE 5'-phosphate oxidase.
Agrobacterium tumefaciene (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA; 23300 MW; 0BADE4CD312327EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
65.2%; Score 45; DB 5; 72.7%; Pred. No. 3.2; cive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AP003011, BAB53553.1; -.
InterPro, IPR00059, Pyridox_oxidase.
Prom, PF01243, Pyridox_oxidase, 1.
ProDom, PD006112, Pyridox_oxidase; 1.
TIGRPAMS, TIGR00558; pdxH; 1.
PROSITE; PS01064; PYRIDOX_OXIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium loti (Mesorhizobium loti)
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2001 (TrEMBLrel. 18, Created U-OCT-2001 (TrEMBLrel. 14, Last st 01-UTN-2002 (TrEMBLrel. 21, Last at Pyridoxamine 5'-phosphate oxidase.
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Gaps

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SEQUENCE FROM N.A.
STRAIN=16M / ALCC 23456 / BIOTYPE 1;
STRAIN=16M / ALCC 23456 / BIOTYPE 1;
MEDLINE=20020109; PubMed=11756689;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyva A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R., O'Callaghan D., Letesson J.-J., "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";

Natl. Acad. Sci. U.S.A. 99:443-448(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dycopersicon esculentum (Tomato).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Brucellaceae, Brucella.
NCBL_TaxID=29459;
                                                                                                   Length 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 208;
                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                 01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5).
BMEII517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
  TIGRFAMS; TIGRO0558; pdxH; 1.
PROSITE; PS01064; PYRIDOX OXIDASE; UNKNOWN_1.
Oxidoreductase; Complete proteome.
SEQUENCE 206 AA; 23900 MW; A2DB74229DACA97A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS01164; PYRÍDOX OXIDASE; 1.
Oxidoreductase; Complete Proteome.
SEQUENCE 208 AA; 23866 MW; CB1F50BC9612DE28 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 16;
Pred. No. 5.5;
1; Mismatches 4,
                                                                                               62.3%; Score 43; DB 16; 58.3%; Pred. No. 5.5;
                                                                                                                                                                                                                                                                                                                          208 AA
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                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:443-4
EMBL; AE009587; AAL52698.1; -.
Incerro; IPR006569; Pyridox.oxidase.
Pfam; PF01244; Pyridox.oxidase; 1.
ProDom; PD006312; Pyridox.oxidase; 1.
TIGRFAMS; TIGR00558; pdxH; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.3
Best Local Similarity 58.3
Matches 7, Conservative
                                                                                                                                         7; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CFHWKSLRROVR 101
                                                                                                                                                                                1 CFQWKRAMRKVR 12
                                                                                                                                                                                                                      88 CFHWKSLRROVR 99
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                                                                                                                      Best Local Similarity
Matches 7; Conserv
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                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                             OBYFK3
                                                                                                                                                                                                                                                                                                                       Q8YFK3
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDIJNB=2160851; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Goodner B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CSB.",
Science 294:2323-2328(2001).

EMBL, AE009043; AAL4176.1, -
                                                MEDLINE-21668550, PubMed=11743193;

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,

Okura V.K., Zhou Y., Chen L., Wood G.E., Almada N.F. Jr., Woo L.,

Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr.,

Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,

Kutyavin I., Levy R., Li M.-J., McClalland E., Palmieri A.,

Raymond C., Rouse G., Senphimmachak C., Wu Z., Romero P., Gordon D.,

Zhang S., Yoo H., Tao Y., Bidlle P., Jung M., Krespan W., Perry M.,

Chundley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,

Nester E.W.;

Whe genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         092RH8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase) protein
PEC 1.43.3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62.3%; Score 43; DB 16; Length 206; 58.3%; Pred. No. 5.5; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 206 AA; 23720 MW; 3BE488AE5307C0C1 CRC64;
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Science 294:2317-2323(2001).
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NCBI_TaxID=176299;
                                    SEQUENCE FROM N.A.
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**Q92RH8** 

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Indels

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Mismatches Pred. No.

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7; Conservative
 Best Local Similarity
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Q9XFD5;
                                                                                                                                              017772
                                                                                                                    RESULT 11
017772
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                 Matches
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                                                        "Characterization of the gene encoding the apoprotein of phytochrome B2 in tomato, and identification of molecular lesions in two mutant alleles.";
            Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
Cordonnier-Pratt M.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.9%; Score 42; DB 10; Length 1121; 54.5%; Pred. No. 44; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGR00229; sensory box; 2.
PROSITE; PS00061; ADH SHORT; UNRNOWN 1.
PROSITE; PS00245; PHYTOCHROME 1. 1.
PROSITE; PS0046; PHYTOCHROME 2; 1.
SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 2.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11709;
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                                                                                                               InterPro; IPR002198; ADH short.
InterPro; IPR002594; APPbind_ATPase.
InterPro; IPR003018.
                                                                                                                                                        Interpro; IPR003018; GAF.
Interpro; IPR003018; GAF.
Interpro; IPR004359; HIS_KINA.
Interpro; IPR004359; HIS_KINA.
Interpro; IPR001510; PAC.
Interpro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF01518; HATPage_c; 1.
                                                                                                  Mol. Gen. Genet. 261:901-907(1999).
EMBL; AF122901; AAD50631.1; -.
MEDLINE=99413290; PubMed=10485280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IRR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
NON TER 508 508
                                                                                                                                                                                                                                                                                             Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                    SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase c; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                           PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                         PRINTS; PR01033;
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ENV.
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SEQUENCE
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Q74118;
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74118
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DB 15; Length 508;

Score 41;

59.48;

Query Match

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                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (Fragment).
Cytochrome P450 (Fragment).
Syerativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Liu J., Yang J.,
Liu J., Yang J.
"Suppression subtractive hybridization (SSH) identified candidate
genes that are differentially expressed at rice young panicle.";
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Science 282:2012-2018[1998].
Science 282:2012-2018[1998].
Science 282:2011 (Calponin-like.)
InterPro; IPR0001715; Calponin-like.
InterPro; IPR0001936; RasGAP.
InterPro; IPR0001936; RasGAP.
Remi; PF00612; IQ; 1.
Prom; PF00612; IQ; 1.
SMART; SM00013; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1391;
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PROSITE; PS50018; RAS GTPASE ACTIV 2; 1.
SEQUENCE 1391 AA; 159210 MW; 794DF9EBFA2E65AC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Lennard N.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.4%; Score 41; DB 5; 70.0%; Pred. No. 83; iive 1; Mismatches
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                                                                                                                                                  PRT, 1391 AA.
                                                                                                                                                                                         Created)
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                    01-07N-1998 (TrEMBLrel. 05, 01-07N-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, F09C3.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                               PRELIMINARY;
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Caenorhabditis elegans.
                      340 KWKEAMREVR 349
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Best Local Similarity
3 QWKRAMRKVR 12
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TISSUE=TESTIS;
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Q96M21
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Van der Loeff, Whittle H., Breuer J.;
Mortality among human immunodeficiency virus type 2-positive
J. Villagers in rural guinea-bissau is correlated with viral genotype.";
J. Virol. 72:7895-7899(1998).
EMBL, Addless, CAAO9580.1;
InterPro, IPRO0077, GP120.
Pfam; PRO0516; GP120;
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MEDLINE=97255645; PubMed=9100992;
Xiang Z., Ariyoshi K., Wilkins A., Dias F., Whittle H., Breuer J.;
"HIV type 2 pathogenicity is not related to subtype in rural guinea
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Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-- In MILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL, AF1404986; AAD29699.1; --
InterProj. IPR001128; Cytochrome_P450.
                                                                                                                                                              SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 AA; 14891 MW; 24882B768F66F88B CRC64;
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Last annotation update)
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Viruses, Retroid viruses, Retroviridae, Lentivirus
NCBL_TaxID=11709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bissau.";
AIDS Res. Hum. Retroviruses 13:501-505(1997).
                                                                       Pfam; PF00067; p450; l.
PRINTS; PR00385; P450.
PROSITE; P500086; CYTOCHROME P450; UNKNOWN l.
Heme; Monooxygenase; Oxidoreductase.
lon Tex
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(TrEMBLrel. 12, I
(TrEMBLrel. 20, I
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nes 6; Conservative
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72 EWKRAMQEVK 81
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                                                                                                                                                                                                                                                                               Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C., "Molecular cloning of 11S globulin and 2S albumin, the two major seed
Sesamum indicum (Oriental sesame) (Gingelly).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
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Q96M21;
Q1-DEC-2001 (TERMELrel. 19, Created)
O1-DEC-2001 (TERMELrel. 19, Last sequence update)
O1-DEC-2001 (TERMELrel. 19, Last annotation update)
CDNA FLJ32891 fis, clone TESTI2004929.
Endo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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J. Agric. Food Chem. 47:4932-4938(1999).

EMBL. AF091841; AAA42943.1;
InterPro; IPR003612; AAI.
InterPro; IPR001612; AAI.
InterPro; IPR001768; Try/amyl inhbtr.
Fram; PR00234; tryp_alpha_amyl; 1.
SPRINTS; PR00499; NAI; 1.
SEQUENCE 148 AA; 17524 MW; BA46B033BA13B3DE CRC64;
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Pred. No.
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Human, lactoferrin, modification, infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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AAY78049
AAY78036
AAY78050
AAY78051
AAY98554
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AAY78031
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AAY78034
AAY78066
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AAR69352
AAW13397
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AAR44841
AAR48530
AAR48531
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AAR84698
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AAR80264
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AAR91852
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AAR87622
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98SE-0002562.
98SE-0004614.
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AAY78094;
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56.918 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAY78070
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through actoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal uninary tract inflammations and/or tumours. The peptides can also be used as unit and an infant formula food. The peptides can also be used as preservatives. The peptides are also continual and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                  Claim 22; Page 38; 102pp; English
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AAY78001 to AAY78100 represent peptides having sequences based on human

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflemmations, colltis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment ourinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                     Score 66; DB 21; Length 12; Pred. No. 0.00014;
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                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78091 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                                                        12 AA;
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferzin. The peptides are taken up in the intestine through binding to specific lactoferzin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungleidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used alinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, lactoferrin, modification, infection, inflammation; tumour; food, infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
fungicidal and bactericidal and may also be used as preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                   Score 65, DB 21; Length 12;
Pred. No. 0.0002;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              AAY78092 standard; Peptide; 12 AA.
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                                                                                                                                                                                     92.9%;
91.7%;
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98SE-0004614.
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                                                                                                                                                                               92.9
Best Local Similarity 91.7
Matches 11, Conservative
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                                                                                                                                                 12 AA;
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as mebrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all initically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                            Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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83.3%; Pred. No. 0.00095;
tive 1; Mismatches 1; Indels
                                         92.9%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 0.0002; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                AAY78038 standard; Peptide; 12 AA.
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                                            Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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98SE-0004614.
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Best Local Similarity
Matches 10; Conserv
                12 AA;
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29-DEC-1998;
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              Seguence
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AAY78038
ID AAY78
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anti-tumour;

Human, lactoferrin, modification, infection, inflammation, tumour, food; infant formula, anti-inflammatory, anti-microbial, anti-tumou urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.

Human lactoferrin derived peptide SEQ ID NO:47.

(first entry)

25-APR-2000

AAY78047;

AAY78047 standard; Peptide; 12 AA.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides are also in food sulfs such as infant formula food. The peptides are also sungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, lactoferrin, modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                       AAY78046 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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1 CFAWKRNMRKVR 12
                                    WPI; 2000-147388/13.
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17-JUL-1998;
29-DEC-1998;
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 73; 102pp; English.

Dolphin GT;

Mattsby-Baltzer I, Baltzer L,

WPI; 2000-147388/13.

Hanson LA,

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1.

Homo sapiens. Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferzin. The peptides are taken up in the intestine through binding to specific lactoferzin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for traating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections (such as uncobal can be used for tracting and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferzin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferzin would canble them to be used for the same purposes as lactoferzin at lower
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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ID AAY7
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AC AAY7
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DT 25-A
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DE Huma
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1 CFAWKRNMRKVR 12

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RESULT 7

Dolphin GT;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungleidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, Jactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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83.3%; Pred. No. 0.001;
cive 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                                                                                                                            Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                               99WO-SE01230.
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
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                                          WO200001730-A1.
                                                                                                                                                                        06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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                                                                                     13-JAN-2000.
Synthetic.
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              Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
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Pred. No. 0.00095;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 22; Page 36; 102pp; English.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.33,
Best Local Si Conservative
                                                                                  pactericidal; preservative
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                                                                                                                               Homo sapiens
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29-DEC-1998;
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                                                                                                                                                     Synthetic.
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RESULT 9
AAY78037
ID AAY778037
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DT 25-A'X
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KW Human
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KW FUMM
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Hanson LA, Mattsby-Baltzer I,
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                             13 AA;
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29-DEC-1998;
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                                                                                                                                                                                          AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used to suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. The republication and infections and infections and arti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anci-inflammatory; anci-microbial; anci-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                 New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.001;
1; Mismatches 1; Indels
                                                                                   Dolphin GT;
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                                                                                 Baltzer L,
                                                                                                                                                                     Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78049 standard; Peptide; 13 AA.
                                                                                 Mattsby-Baltzer I,
         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                       87.1%;
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98SE-0002562,
98SE-0004614.
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Best Local Similarity 83.3'
Matches 10; Conservative
                                                        (ASCI-) A+ SCI INVEST AB
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                                                                                                        WPI; 2000-147388/13.
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         06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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                                                                                 Hanson
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as writhary tract infections, colitis, and Candida infections (such as writhary tract infections, colitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also the fungicidal and bactericidal and may also be used as preservatives.

Bren though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                               New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
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Pred. No. 0.001;
1; Mismatches 1; Indels
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Dolphin GT;
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Baltzer L,
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98SE-0004614
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Query Match
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ID AAY
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
bactericidal; preservative.
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Claim 12; Page 69; 102pp; English.
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                                                                                                                                                                                                                                               87.18;
83.38;
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98SE-0002562.
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                                                                                                                                                                                                                                                                      10; Conservative
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                                                                                                                                                                                                                                                                                               1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                             3 CFQWQRNMRKVR
                                                                                                                                                                                                                       14 AA;
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29-DEC-1998;
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                                                                                                                                                                                                                       Sequence
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urrinary tract infection; colltis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.1%; Score 61; DB 21; Length 14;
83.3%; Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltzer L,
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98SE-0002562.
98SE-0004614.
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nes 10; Conservative
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17-JUL-1998;
29-DEC-1998;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.
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                                                                             Query Match 87.1%; Score 61; DB 21; Length 14; Best Local Similarity 83.3%; Pred. No. 0.0011; Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                          anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-ulcer agent contg. peptide - has low toxicity, is heat-resistant and water-soluble
                                                                                                                                                                                                                                AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                Peptide for anti-ulcer agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94JP-0283869.
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                                                                                                                                    1 CFAWKRNMRKVR 12
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                                                     14 AA;
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Gaps

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Query Match 87.1%; Score 61; DB 17; Length 15; Best Local Similarity 83.3%; Pred. No. 0.0012; Matches 10; Conservative 1; Mismatches 1; Indels

Sequence 15 AA;

1 CFAWKRNMRKVR 12 || |:|||||| 2 CFQWQRNMRKVR 13

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Search completed: February 21, 2003, 07:56:44 Job time: 28.093 secs

AAR98531-54 are peptides used in an anti-ulcer agent. The agent is low in toxicity, is heat-resistant and stable in aqueous soln.. It can be administered orally and be produced in large amounts.

Claim 1; Page 11; 11pp; Japanese.

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Sequence
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Sequence
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                                                                                                                                                                                                                                                                                                                                    APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICERAL
APPLICANT: TANAKA, SHICERAL
APPLICANT: DOSAKO, SHIN'ICHI
APPLICANT: MAMASAKI, YOSHIHIRO
APPLICANT: UTULDA, TOSHIKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: S3 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk

COMPUTER: IPM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS.

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487

FILING DATE: 02-MAR-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: CAMPBELL, PAULA A.

REFERENCES/DOCKET NUMBER: FJN-019

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                         US-09-265-577-2
                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDKEL: 53 CITY: BOSTON MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: BOS
STATE: MA
COUNTRY:
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US-08-204-487-3
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 25,
Sequence 24,
Sequence 25,
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Sequence 10,
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Sequence 7,
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Sequence 8,
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Sequence 3,
Sequence 1,
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Sequence
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-264-711-24
US-08-256-771-25
US-08-256-771-25
US-08-31-984-24
US-08-31-984-24
US-09-508-734-4
US-09-508-734-4
US-09-508-734-6
US-07-755-161A-10
US-09-508-734-8
US-07-991-174-8
US-07-891-174-8
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 CFAWKRNMRKVR 12
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Match Length
                                                                                                                                          score:
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Perfect
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No.
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Sequence 8, Application US/08475055
Patent No. 5962245
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APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS
TITLE OF INVENTION: BUDENOD
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-628-380-8
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Best Local Similarity 83.3
Matches 10; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA;
APPLICANT: ANTHORMATION:
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
                                                                                                          Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                               Score 61; DB 1; I
Pred. No. 0.00072;
1; Mismatches 1;
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Pred. No. 0.00072;
1; Mismatches 1.
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATVORBY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELEPRINCE/DOCKET NUMBER: 947-1-00
TELEPRINCE/DOCKET NUMBER: 947-1-00
TELEFRINE: 201 487-5800
                                                                                                                                                                                                                                                                            Sequence 8, Application US/08485948
Patent No. 5855882
, OTHER INFORMATION: (20-37)"
US-08-204-487-3
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ilarity 83.3%;
Conservative
                                                           Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FRACMENT TYPE: internal
US-08-485-948-8
                                                                                                                                         1 CFAWKRNMRKVR 12
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Matches 10; Conservat
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US-UD-268-300
PRESENT NOTE OF SEQUENCE BY APPLICATION US/08628380
PRESENT N. FORMATION:
FROMETON:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 2;
Pred. No. 0.00072
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IOCATION: 19
IOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
THEORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.1%; Score 61; DB 1; Length 20;
                                                                       US/07/755,161A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE:

DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-3
                                                                                  FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
RAME: WARTEN TON TONER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KET: modified site
LOCATION: 2
LOCATION: 2
LOCATION: 7
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys ree
OTHER INFORMATION: thiol g
FRATURE:
                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO: 3;
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                              SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 87.1%; Score 61; DB 2; Length 18; Best Local Similarity 83.3%; Pred. No. 0.00072; Matches 10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

STREET: D.C.
STREET: D.C.
                                                                                                                                 COMPUTER YOUNG TERMS AND THE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 SOFTWARE: PAPLICATION NUMBER: US/08/475,055 FILING DATE: PRIOR APPLICATION:
PRIOR APPLICATION: DATA: APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 06/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 06/418,642
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 947-1-0
TELECOMMUNICATION INFORMATION:
TELEPRAN: 201 487-5800
TELEPRAN: 201 343-1684
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEK: 133521
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                New Jersey
: USA
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                                                          CITY.
STATE: Ne.
COUNTRY: USA
7. 07601
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LOCATION: 2

LIBENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cyg residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cyg residue at location 19"

NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
LOCATION: Cyg residue at location 19 connected by disulfide bond with OTHER INFORMATION: Cyg residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cyg residue at location 2"
AUTHORS:
TITLE:
TITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHINYO
APPLICANT: KAWASAKI, YOSHININO
APPLICANT: UCHIDA, TOSHIAKI
TITLE OF INVENTION: URBL. INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61; DB 1; Length 20;
Pred. No. 0.00079;
1; Mismatches 1; Indels
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COUNTRY: USA
ZIP: 02109
COMPUTRY: USA
ZIP: 02109
COMPUTRY: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIF/CATTON:
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NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAGES:
DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08204487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAMAMOTO, NAOKI
NAKASHIMA, HIDEKI
MOSUCHI, WATARU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPAWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-204-487-1
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                                      Gaps
                                      Indels
                                                                                                                                                                                                                               RESULT 6
US-07-891-174-3
; Sequence 3, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
APPLICANT Mamoru TOMITA et al.
ITILE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
MUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fitteenth Street, N.W., #700
Best Local Similarity 83.3%; Pred. No. 0.00079;
Matches 10; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.25 inch, 500Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 5(
COMPUTER: IBM Compatible

OPERATING SYSTEM:

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/891,174

FILING DATE: 29-MAY-1992

CLASSIFICATION NUMBER: US/07/891,174

FILING DATE: 05-SEP-1991

APPLICATION NUMBER: US/07/55,161

FILING DATE: 05-SEP-1991

ATTORNEY/AGENT INFORMATION:

NAME: WALFER M. CHERK J. SEET STREET STREET NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELERPHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 antino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
CREGINAL SOURCE:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITS:
FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEAIN:
INDIVIDUAL ISOLATE:
BEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL ILWE:
ORGANELLE:
IMMEDIATE SOURCE:
LIERRY:
CLONE:
CLONE:
                                                                                    1 CFAWKRNMRKVR 12
                                                                                                                           2 CFOWORNMRKVR 13
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CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.
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Gapa
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Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mannoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are protected to OTHER INFORMATION: prevent disulfide bond"
US-08-256-771-25
                                             Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61, DB 1, Length 20;
Pred. No. 0.00079;
1; Mismatches 1; Indels
                                             Score 61; DB 1; ]
Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005 D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: U1y 22, 1994
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700
CITY: Washington
                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                             Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                               1 CFAWKRNMRKVR 12
                                                                                                                                                                        2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                      RESULT 9
US-08-256-771-25
    US-08-256-771-24
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US-08-381-984-24
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Sequence 24, Application US/08256771

Patent No. 556591

GENERAL INCOME.

TITLE OF INVENTION: ANYIMICROBIAL AGENTS AND METHOD FOR TREATING

TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STREET: 0.C.

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                        87.1%; Score 61; DB 1; Length 20; 83.3%; Pred. No. 0.00079; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                    /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: Ms-DOS SOFTWARE: Mordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: Unly 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEPHONE: 202-371-8850
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEGURATE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TELEFAX: (617) 248-7100 INPOMMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids:
                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                   Query Match.
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                          LOCATION: 1..20
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 CFQWQRNMRKVR 13
                                                                                                                                                                                          NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                          1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                             US-08-204-487-1
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RESULT 12

US-09-508-734-4

is Sequence 4, Application US/09508734

is Sequence 4, Application US/09508734

is Patent No. 6423509

is GENERAL INFORMATION:

APPLICANTY Samyang Genex Corporation

TITLE OF INVENTION: Useful microorganism thereof

TITLE OF INVENTION: USO 00139

CURRENT FILING DATE: 2000-06-01

FRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
| LOCATION:
| LOCATION NETHOD:
| TIBRNITECATION METHOD:
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkag US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
LOCATION:
TIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.00079;
1; Mismatches 1; Indels
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
RILING DATE:
               805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide FEATURE:
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            STREET: 805 Fifte
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                 : D.C.
RY: U.S.A.
20005
                                                                                  COUNTRY:
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LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thered
US-08-381-984-24
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LOCATION:
IDENTIFICATION METHOD:
CTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.1%; Score 61; DB 1; Length 20; 83.3%; Pred. No. 0.00079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
Sequence 24, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
    APPLICANT: Mamoru TOMITA et al.
    TITLE OF INVENTION: ANTIOXIDANT
    NUMBER OF SEQUENCES: 32
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Wenderoch, Lind & Ponack
    STREET: 805 Fifteenth Street, N.W., #700
    CITY: Washington
                                                                                                                                                                                                                                            STATE: D.C.
COUNTX: U.S.A.
21P: 2000
COMPUTEX: U.S.A.
21P: 2000
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIPICATION 2478:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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; Patent No. 5804555;
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT;
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.3
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-381-984-25
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TELEX:
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POSITION IN GENOME:
CHLONE:
CHROMOSOMS/SEGMENT:
MAP POSITION:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
FEATURE:
NAME/KEY: modified site
LOCATION: 21"
FEATURE:
NAME/KEY: modified site
LOCATION: Cys residue at location 21"
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION: thiol group of Cys residue at location 4"
MUTHERS:
MAUTHERS:
MATHERS:
MAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
        FILING DATE:
ATORNEY/AGENY INFORMATION:
NAME: WALTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE//DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acida
TYPE: AMINO ACID
STRANDEDRESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                        TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
INDIVIDAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFAWKRNMRKVR 12
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ઠે
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; Patent No. 6423509
; Patent No. 6423509
; Patent No. 6423509
; Patent No. 6423509
; Patent No. Caporation
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and
; TITLE OF INVENTION: UNDERS. US/09/508,734
; FILE REFERENCE: PA/SYG/00139
; CURRENT FALING DATE: 2000-06-01
; PRIOR FILING DATE: 1999-07-14
; PRIOR FILING DATE: 1999-07-14
; PRIOR FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 6
; LENGTH: 24
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                                                                                                                                                                                                           Length 22;
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US-07-755-161A-10
Sequence 10, Application US/07755161A
Sequence 10, Saplication US/07755161A
Sequence 10, Sald633
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: DisplayWrite
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
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                                                                                                                                                                                                   Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity 83.3
Matches 10; Conservative
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PRIOR APPLICATION DATA
APPLICATION NUMBER:
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                1 CFAWKRNMRKVR 12
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Search completed: February 21, 2003, 08:04:27 Job time : 8,93023 secs
                                                                                                                                                                                                                                                         FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
IDENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: CYS
OTHER INFORMATION: thic
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                              Query Match 87.1
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                        DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                       US-07-891-174-10
                                                                                                                                      JOURNAL:
VOLUME:
ISSUE:
                                                                                                                                                                                                  PAGES:
DATE:
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UNITES:
DAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                     Sequence 10, Application US/07891174
; Sequence 10, Application US/07891174
; Patent No. 5317084
; GENERAL INFORMATION:
    APPLICANT: Mamoru TOMITA et al.
    TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Wenderoch, Lind & Ponack
    STREET: 805 Fifteenth Street, N.W., #700
    CITY: Washington
    STATE: D.C.
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                             COMPUTE: 20005
COMPUTE: READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
OUNDITE: IBM Compatible
OUNDITE: IBM Compatible
OURRENT MEDIATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NUMBER: US/07/891,174
FILING DATE: 05-MAY-1992
ATORNEY/AGENT INFORMATION:
NAME: WARTEN MY Cheek Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
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21
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT:
MAP POSITION:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
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MOLECULE TYPE:
HYPOTHETICAL:
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NAME/KEY:
LOCATION:
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/note= "thiol group of
Cys residue at location 21 connected by disulfide bond with
thiol group of Cys residue at location 4"
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0
                                                                                                                                                                                                                                                                                                                                 Length 25;
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us-09-743-107b-94.rapb

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, APPLICANT: BALDUR SVEINBJ (RNSSON
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                                                                                          February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 24,
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Sequence 26,
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Sequence 11
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/ cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.psp:*
/ cgn2_6/ptodata/2/pubpaa/NCT NEW PUB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/NEO7_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/NEO7_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.psp:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.psp:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications AA:*
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                     US-09-743-107B-94
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Maximum DB seq length: 2000000000
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Match Length
                                                                                                                                                            Title:
Perfect score:
Sequence:
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                                                                                              Run on:
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No.
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Sequence 30, Appl Sequence 28, Appl Sequence 28, Appl Sequence 4,002, A Sequence 7, Appli Sequence 8, Appli Sequence 20, Appli Sequence 30, Appli Sequence 31, Appli Sequence 38, Appli Sequence 3754, Appli Sequence 1424, Appli Sequence 1515, Appli Sequence 1515, Appli Sequence 1515, Appli		ength 15; Indels 0; Gaps 0;
US-09-981-649A-30 US-09-981-649A-32 US-09-981-649A-28 US-09-981-649A-28 US-09-864-761-41002 US-09-798-869-30 US-09-798-869-30 US-09-510-332-68 US-09-510-332-68 US-09-510-332-68 US-10-121-049-38 US-10-121-049-38 US-10-121-049-38 US-10-1176-9138 US-09-925-301-1248 US-09-913-585-50 US-09-913-585-50 US-10-111-911-1	ALIGNMENTS 798869 A1 SEN NSSON 18A-A US/09/798.869 2-27 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851 1.1/GB99/02851	ore 61; DB 9; L ed. No. 0.00026; Mismatches 1; 69
7.7.7.6.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.4.	Cation US/0979886 IS20030022821A1 ON: SIGURD SYENDEN FIN REKDAL ON: BIOACTIVE PEP (NO STANDAL ON: BOACTIVE PEP A34049-PCT-USA-A A74E: 2001-02-27 NN UNMBER: GE98189 E: 1999-08-31 E: 1999-08-31 E: 1998-08-38 NN UNMBER: GE98189 NN UNMBER: GE98189 NOS: 30 O for Windows Ver	Scrit; SC   Conservative   1; SC   Conservative   1; SC   Scritt   1; SC   SC   Scritt   1; SC   SC   SC   SC   SC   SC   SC   SC
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Gaps
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0
Score 61; DB 9; Length 694;
Pred. No. 0.01;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 53, DB 9, Length 15, Pred. No. 0.0056; 1, Mismatches 2; Indels
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US-09-798-809-3
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: UCHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIDACTIVE PEPTIDES
FILE REPRESENCE: A3409-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR PILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR FILING DATE: 1998-08-31
SROID NOS: 30
SOFTWARE: FRANKER FRANKER FRANKER FRANKER FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR FILING DATE: L998-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR APPLICATION NUMBER: G39818938-4
PRIOR FILING DATE: L998-08-31
                                                                                                                                                                                                                                                                                                                    Geguence 6, Application US/09798869
Squence 6, Application US/09798869
Publication No. USZ0030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: JALDUR SVEINBAL
TITLE OF INVENTION: BIOACTURE PEPTIDES
TITLE OF INVENTION: BIOACTURE PEPTIDES
TITLE DE INVENTION: BIOACTURE PEPTIDES
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR PEPLICATION NUMBER: PCT/GB99/02851
PRIOR PELING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRACES
SEC ID NO 6
SEC ID NO 6
SEC ID NO 6
SEC ID NO 6
SED ID NO 6
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75.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 9; Conservative
      Query Match
Best Local Similarity 83.3
Matches 10; Conservative
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Best Local Similarity
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ORGANISM: CAPRINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Tomasz
APPLICANT: Sollnick, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Doyle, Darrell J.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS MS-DOS
SOFTWARE: PC-DOS MS-DOS
SOFTWARE: PC-DOS MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 61; DB 9; I
Pred. No. 0.00043;
L; Mismatches 1;
                         AFTLANI: LARS VOLUMENTON: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICEATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US/08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P5816
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFAWKRNMRKVR 12
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APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Milennium Pharmaceuticals, Inc.
APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
ITILE OF INVENTION: 80090, 52874,52880,63497, AND 33425
ITILE OF INVENTION: METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF
ITILE OF INVENTION NUMBER: US/10/080,960
CURRENT APPLICATION NUMBER: US 60/242,040
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/242,038
PRIOR PILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: US 60/241,992
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: US 60/242,637
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 301
TYPE: PRT
ORGANISM: Homo sapiens
                                                                       NE FILING DATE: 1999-09-30
OR APPLICATION NUMBER: 09/471,179
OR APPLICATION NUMBER: 09/471,179
OR FILING DATE: 1999-12-29
OR APPLICATION NUMBER: 09/474,072
OR APPLICATION NUMBER: 09/474,072
OR APPLICATION NUMBER: 09/514,010
OR FILING DATE: 2000-02-25
OR APPLICATION NUMBER: 09/516,745
OR FILING DATE: 2000-03-16
OR APPLICATION NUMBER: 09/516,745
OR FILING DATE: 2000-03-14
OR APPLICATION NUMBER: 09/512,002
OR APPLICATION NUMBER: 09/572,002
OR APPLICATION NUMBER: 09/572,002
OR APPLICATION NUMBER: 09/572,002
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                   PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/405
PRIOR FILING DATE: 1999-09-20
PRIOR FILING DATE: 1999-12-23
PRIOR FILING DATE: 1999-12-23
PRIOR PELING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/47
PRIOR PELING DATE: 1999-12-29
PRIOR PELING DATE: 2000-02-25
PRIOR PELING DATE: 2000-02-25
PRIOR PELING DATE: 2000-02-01
PRIOR PELING DATE: 2000-02-01
PRIOR PELING DATE: 2000-05-14
PRIOR PELING DATE: 2000-05-14
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PRIOR PELING DATE: 2000-05-20
PRIOR PELING DATE: 2000-05-20
PRIOR PELING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
LENGTH: 333
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Best Local Similarity 54.5
Matches 6; Conservative
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; ORGANISM: Mouse
US-09-796-753-26
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  Gaps
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Lthy, Sean A.

LION: SECRETED PROTEINS AND USES THEREOF

LICATION NUMBER: US/09/796,753

FILING DATE: 2000-03-01

APPLICATION NUMBER: 09/83,175

LOR APPLICATION NUMBER: 09/23,094

PRIOR PILING DATE: 1998-10-30

NOR APPLICATION NUMBER: 09/223,546

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: PRIOR PILING DATE: PRIOR PILING DATE: PRIOR PILING DATE: PRIOR PILING DATE: PRIOR PILING PAPELICATION NUMBER: PRIOR PILING PAPELICATION PRIOR PIT
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  2; Indels
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Pred. No. 0.28;
3; Mismatches
                                                                                                                                                                                                                                                                                                 APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN PERDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACITYE PERTIDES
CURRENT APPLICATION NUMBER: US/09/798,865
CURRENT APPLICATION NUMBER: US/09/798,865
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GP9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESERE FOR WINDOWS VERSION 4.0
SSETURN 25
LENGTH: 25
                                                                                                                                                                                                                            Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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Best Local Similarity 54.5%;
Matches 6; Conservative
6; Conservative
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                                                                                                3 CYQWQRRWRKL 13
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; ORGANISM: CAPRINE
US-09-798-869-23
Matches
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CURRENT APPLICATION NUMBER: US/09/978,295A
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Krijavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, Audrey
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APPLICANT: Baker Kevin P.
APPLICANT: Betsetin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Paoni, Nich
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; ORGANISM: MURINE
US-09-798-869-22
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US-09-978-295A-119
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100.0%; Pred. No. 14;
iive 0; Mismatches 0; Indels
                                            57.1%; Score 40; DB 9; Length 301; 100.0%; Pred. No. 14;
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                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                    Georgia Constitution US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: GYSTEN REKALL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
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APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANTON NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: ABSTERMENT STATES ADDRESSED FOR WINDOWS NOT STATES ADDRESSED FOR WINDOWS 
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Best Local Similarity 100.0
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                          Query Match
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                     296 CFAWKR 301
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                                                                                                                                      1 CFAWKR 6
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US-10-080-960-11
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ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same 11E REFERENCE: P2630P1C11
Score 39; DB 9; Length 25;
Pred. No. 1.9;
                                                   4; Indels
                                                   1; Mismatches
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PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 2001-07-30
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1997-1. 1993-1. 1993-1. 1997-1. 1997-1. 1997-1. 1998-0. 1998-0. NUMBER: 1998-0. NUMBER: 1998-0. NUMBER: 1998-0.	1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.  1998 - 0.	1998-03-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1 1998-8-1	1998. NUMBER NUMBER 1998. NUMBER 1998. 1998. 1998. NUMBER 1998.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: William J.
APPLICANT: William J.
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC27
CURRENT APPLICATION NUMBE: 105/09/978,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%; Score 39; DB 9; Length 338; 45.5%; Pred. No. 23; indels iive 3; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: 09/91858

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/064249

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-11-13
                                                         PRIOR FILING DATE: 1998-05-15
RRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
                                  LICATION NUMBER: 60/085582
ING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085697
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Gerritsen, Mary E
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Kuo, Sophia S.
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Pan, James;
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Best Local Similarity 45.5
Matches 5; Conservative
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R APPLICATION NUMBER: 00/001015
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APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
APPLICATION NUMBER: 60/08336
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/08332
FILING DATE: 1998-04-27
APPLICATION NUMBER: 60/08332
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FILING DATE: 1998-05-06
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084637
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084639
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PEPLICATION NUMBER: 60/082704
PILING DATE: 1998-04-22
NEPLICATION UNMER: 60/082804
TILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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LICATION NUMBER: 60/083558
NG DATE: 1998-04-29
LICATION NUMBER: 60/083559
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ICATION NUMBER: 60/083742.
NG DATE: 1998-04-30
ICATION NUMBER: 60/084366
LING DATE: 1998-04-15
PLICATION NUMBER: 60/082568
LING DATE: 1998-04-21
PLICATION NUMBER: 60/082569
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ICATION NUMBER: 60/083495
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PLICATION NUMBER: 60/083499
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PLICATION NUMBER: 60/083554
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ICATION NUMBER: 60/083500
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LICATION NUMBER: 60/084414
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PLICATION NUMBER: 60/085582
LING DATE: 1998-05-15
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085689
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APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
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                                                                                                                                                                                                                                         Length 338;
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Pred. No. 23;
3; Mismatches
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CURRENT FILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR PLICATION NUMBER: 60/06220
PRIOR APPLICATION NUMBER: 60/06249
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-03
PRIOR PILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06634
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-21
PRIOR PILING DATE: 1997-11-21
PRIOR FILING DATE: 1997-11-21
                PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
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PRIOR PLING DATE: 1998-05-15
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Patent No. US20020177553A1
GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Nazier, Mary A.
Pan, James;
Paoni, Nicholae F.
Sky, Margaret Ann
Shelton, David L.
Stewart, Timothy A
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Perrara, Napoleon
Pilvaroff, Ellen
FILING DATE: 1998-05-15
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PPLICANT: Baker Kevin P.
PPLICANT: Botstein, David
PPLICANT: Desnoyers, Luc
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Best Local Similarity 45.5
Matches 5, Conservative
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Gao, Wei-Qiang
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PRIOR PRICATION NUMBER: 60/08349
PRIOR PLING DATE: 1998-04-29
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R APPLICATION NUMBER: 60/081070
R FILING DATE: 1998-04-08
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R APPLICATION NUMBER: 60/080107
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R FILING DATE: 1998-04-01
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R APPLICATION NUMBER: 60/079656
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APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/081955
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                                                                                                     Query Match 55.7%; Score 39; DB 9; Length 338; Best Local Similarity 45.5%; Pred. No. 23; Matches 5; Conservative 3; Mismatches 3; Indels
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CURRENT FILING DATE: 2001-10-24
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US-09-99-832A-119
Sequence 119, Application US/0999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Betsein, David
APPLICANT: Desnoyers, Luc
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PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06431
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
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FILING DATE: 1998-03-10
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Pann, James,
Paoni, Nicholas F.
Roy, Mrrgaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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ddard, Audrey
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Kuo, Sophia S.
Napier, Mary A.
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Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/08299
PRIOR FILING DATE: 1998-04-29
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Query Match 55.7%; Score 39; DB 9; Length 338; Best Local Similarity 45.5%; Pred. No. 23; Matches 5; Conservative 3; Mismatches 3; Indels

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Maximum Match 100%
Listing first 45 summaries
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	52.9 236 2 A84686	52.9 289 2 G86403	52.9 306 1 A39654	52.9 413 2 T32831	52.9 500 2 G71633	52.9 502 2 TO1179	37 52.9 513 2 E86156 T14P4.7 protein -	52.9 749 2 A45687	52.9 842 2 T04555	52.9 2700 2 D88450	235 2 E91097 hypothetical	52.1 235 2 A85943	51.4 116 1 QQEBHT hypothetical	51.4 116 2 809523	51.4 236 2 AH0157	51.4 283 2 G98020	ALIGNMENTS		lactotransferrin precursor [validated] - human	N;Alternate names: lactoferrin	s: Homo sapiens (man)	C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000	_	And the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t
30 31 32 33 34 34 36 36 39 40 41 42 42 43 44 44 44 41 1accotran C;Species C;Date: 3 C;Date: 3 C;																			sferrin	te names	: Homo s	1-Mar-19	CTOS :UO	4 4

A)Status: preliminary, translated from GB/EMBL/DDBJ A,Molecule type: mRNA A,Residues: 1-711 <CHO> A; Accession: G01394

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A. Cross-references: EMBL: U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237
R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
Nucleic Acids Res. 18, 5288, 1990
A;Reference number: S11228; MUID:90384839; PMID:2402455
A;Recession: S11228
A;Molecule type: mRNA
A;Residues: 1-148, T', 150-422, C', 424-711 (RBY)
A;Residues: 1-148, T', 150-422, C', 424-711 (RBY)
A;Residues: 1-148, T', 150-422, C', 424-711 (RBY)
A;Residues: 1-148, T', 150-422, C', 424-711 (RBY)
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A;Residues: 1-148, T', 180-422, T', 180-422, T', 180-422, T', 180-422, T', 180-422, T', 180-422,

A;Molecule type: DNA A;Residues: 1-15 <TEN> A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placenta A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleotide sequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734

A;Accession: S10324

A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA A; Residues: 3-711 <POW> A; Cross-references: EMBL:XS2941; NID:g34411; PIDN:CAA37116.1; PID:g34412 R; Stowell, K.M.; Rado, T.A.; Punk, W.D.; Tweedie, J.W. Biochem. J. 276, 349-355, 1991 A; Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A; Reference number: S15853; MUID:91264786; PMID:2049066 A; Accession: S15853

A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2> A;Molecule type: mRNA A;Residues: 20-31 <ST1>

Gaps

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4; Indels

Length 511

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Cispecies: Capra aegagrus hirous (domestic goat)
Cispecies: Capra aegagrus hirous (domestic goat)
Cispate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
Ciscession: UC2323
Richem. Biophys. Res. Commun. 203, 1324-1332, 1994
A; Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant lay. Reference number: UC2323, MUID:94380047; PMID:8033048
A; Reference number: UC2323, MUID:94380047; PMID:8033048
A; Reference number: UC3233, MUID:94380047; PMID:8033048
A; Residues: 1-708 < LEP>
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin repeat homology < TRH2>
F; 252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                      A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176 C;Genetics: A;Gene: STX3070
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Pred. No. 2.5;
0; Mismatches
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Best Local Similarity 66.7%;
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A) Cross-references: GDB:119368; OMIM:150210
C) Superidamily: transferrin; transferrin repeat homology
C) Superidamily: transferrin; transferrin repeat homology
C) Keywords: duplication; glycoproctein; iron binding; milk
F) 2-19/Domain: signal sequence #status predicted <SIG>F) 20-11/Product: lactotransferrin repeat homology <TRHI>F) 2-56/Domain: transferrin repeat homology <TRHI>F) 2-55,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,39-56,3
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
G;Accession: AB0858
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fairar, S.; Moule, S.; O'Gaora, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Itle: Complete genome sequence of a multiple drug resistant Salmonella enterica serovals enterica serovals.
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Visities: not compared with conceptual translation
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Visities: al-701, SWKPVN <-PAN>
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Visities: al-701, SP-66, SP-66, SP-701, SP-70
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;Nosecules: 20-140.142:19.00,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4;Note: this is the final paper in a series;
;Houen, G:; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
urr. J. Blochem: 241, 303-308, 1996
fiftle: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin;Reference number: S74119; MUID:97054624; PMID:8898921
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A; Residuas: 436-487, 4, 489-711 <RAD>
A; Crosd-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A; Title: A61169; MUID:91235214; PMID:1674448
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Filte: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
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larity 83.3%; Pred. No. 0.008;
Conservative 1; Mismatches 1; Indels
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Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
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Best Local Similarity
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A;Molecule type: DNA
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assignment of the relevant lo-

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3-deoxy-manno-octulosonate cytidylyltransferase (BC 2.7.7.38) [similarity] - Helicobau C; Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000
C;Accession: E64639
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKeison, D.; Meidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-393 <TOM> A;Residues: 1-393 <TOM> A;Residues: GB:AE000604; GB:AE000511; NID:g2314086; PIDN:AAD08000.1; PID:g231.
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C;Superfamily: Chlamydia trachomatis 3-deoxy-manno-octulosonate cytidylyltransferase
C;Keywords: nucleotidyltransferase
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62.9%; Score 44; DB 2; Length 708; 54.5%; Pred. No. 7.6;
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llarity 45.5%; Pred. No. 6.6;
Conservative 6; Mismatches 0; Indels
                                                                            Indels
                                                                               3; Mismatches
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Gaps

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C;Species: Ureaplasma urealyticum
C;Species: Us-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: B32921
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
eubmitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a m A;Reference number: A82870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <GLA>
A;Cross-references: GB:AE002120; GB:AF222894; NID:g6899167; PIDN:AAF30624.1; GSPDB:GNO
A;Experimental source: serovar 3; biovar 1
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C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C;Accession: D33876
C;Accession: D33876
R;Kodelja, V.; Lucas, K.; Barnert, S.; von Kleist, S.; Thompson, J.A.; Zimmermann, W. J. Biol. Chem. 264, 6906-6912, 1989
A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis A;Reference number: A33876; MUID:89214106; PMID:2708349
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hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupon) C59pcthetical protein tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH3147
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C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
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                                                                              Length 267;
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                                                                                                                                   3; Indels
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                                                                              Score 40; DB
Pred. No. 15;
2; Mismatches
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Pred. No.
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                                                                              57.1%;
58.3%;
                                                                              Query Match
Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A, Residues: 1-114 < KOD>
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42 FAWYRGLRKI 51
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A;Gene: pkn; UU216
A;Genetic code: SGC3
C;Genetics:
A;Genetic code: SGC3
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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C)Accession: S77802
R;Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiold A;Reference number: S77739; MUID:96059641; PMID:7476192
                                                                      C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: S52107; MUID:95127729; PMID:7627104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: S77802
A;Status: nucleic acid sequence not shown; translation not shown
A;Actus: nucleic acid sequence not shown; translation not shown
A;Residues: 1-267 <BOR>
A;Residues: 1-267 <BOR>
A;Cross-references: EMBL: 233006
A;Experimental source: ATCC 27743
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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A;Molecule type: DNA
A;Residues: 1.584 «STO»
A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Vng1732c [imported] - Halobacterium sp. NRC-1
C,Species: Halobacterium sp. NRC-1
C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Species: Mycoplasma capricolum _
C,Date: 09-0ct-1997 #sequence_revision 31_0ct-1997 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                  C, Superfamily: transferrin; transferrin repeat homology C; Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 41; DB 2;
45.5%; Pred. No. 1.5;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2;
Pred. No. 21;
4; Mismatches
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Best Local Similarity 41.7
Matches 5, Conservative

    sheep (fragment)

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                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-33 <QIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFAWKRNMRKV 11
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                                                       actoferrin
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Matches
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Gaps

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Gaps

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C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-May-2002
C;Accession: AG3441
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable pyridoxamine-phosphate oxidase (EC 1.4.3.5) [imported] - Brucella melitensis
    A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41776.1; PID:g17739129; GSPDB:GN00186
A;Cross-reference: strain C58 (Dupont)
C;Genetics:
A;Gene: pdxH
A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-208 «KUR»
A,Cross-references: GB:AE008917; PIDN:AAL52698.1; PID:g17983525; GSPDB:GN00190
                                                                                                                                                                                                                                                                                                                                                                                                                Match 55.7%; Score 39; DB 2; Length 206; Local Similarity 58.3%; Pred. No. 18; to Conservative 1; Mismatches 4; Indels
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C;Superfamily: pyridoxamine-phosphate oxidase
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.3°
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell kranco, P.; Zhang, S. Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pyridoxamine 5'-phosphate oxidase (AF179611) [imported] - Agrobacterium tumefaciens (stricispecies: Agrobacterium tumefaciens (Species: Agrobacterium tumefaciens (Cipate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 (Agrobacterium tumefaciens Signate: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 (Agrobacterium F97451 A) Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A; The Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                ster, E.W.

A)Tile: The General Genetic Engineer Agrobacterium tumefaciens C58.

A)Accession: AH147

A)Accession: Drain ary

A)Accession: Drain ary

A)Accession: AH147

A)Accule type: Drain ary

A)Acc
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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Pred. No. 18;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.5%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 3; Indels
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A,Map position: circular chromosome
C,Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 58.3%;
Matches 7; Conservative
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A;Status: preliminary
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Matches
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Cypecies: Caenorhabditis elegans
Cyptes: 15-Oct-1999 #text_change 04-Mar-2000
Cyptes: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
Cyptes: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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Cyptes: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
Rybotherical type: DAR
AyReference number: 219587
AyReference number: 219587
AyReference: Tail 172597
AyReference: Tail 172597
AyReferences: EMB: 281089; PIDN: CAB03137.1; GSPDB: GN00028; CESP: F53H4.4
AyReference: CBSP: F53H4.4
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                                                                                                    4; Indels
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Score 39; DB 2;
Pred. No. 18;
1; Mismatches
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63.6%; Pred. No.
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Best Local Similarity
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0; Gaps

3; Indels

1; Mismatches

7; Conservative

Matches

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Pyposhetical protein MYPU 5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

Species: Mycoplasma pulmonis

Species: Mycoplasma pulmonis

Species: A-May-2001 #text_change 03-Aug-2001

Species: A-May-2001 #text_change 03-Aug-2001

Chambaud, I.; Heilig, R.; Forris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Mucleic Acids Res. 29, 2145-2153, 2001

Mylitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm; Reference number: A99512; MUID:21267165; PMID:11353084

Mylitle: Preliminary

Molecule type: DNA

Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: Mylitle: M
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Q03278 nasonia vit P26770 rattus norv Q9102 arabidopsis Q24595 drosophila O67763 aquifex aeo Q9x6y2 aquifex pyr P38735 saccharomyc Q9nzm3 homo sapien P38633 homo sapien	Q24048 drosophila P10432 bacteriopha
PO21 NASVI CYA4_RAT ATX1_ARATH XEO_DROWE RPOC_AQUAE RPOC_AQUEY YHD5_YEAST ITM2_HUMAN ABOR_HUMAN	ATB2 DROME YIM9 BPPH1
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Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea
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15-UUL-1999 (Rel. 38, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A;
Lactoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Mammary gland;
MEDLINE-90384839; PubMed=2402455;
Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Mammary gland;
Liang Q., Jimenez-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                     TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; Q00756; Q9H1Z3; Q96KZ4;
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TISSUB=Mammary gland;
TOSUB=Mammary gland;
TOSUB=Mammary bland;
"Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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TISSUBE-Prostate;
Strausberg (R.i.)
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
ALIGNMENTS
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SEQUENCE OF 237-711 FROM N.A.
MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Ghod L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.,
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Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis
and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                         "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                         PREJIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE-82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                               Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J., Jolles P.,
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MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
                                                                                  EEQUENCE OF 20-711.
MEDLINE-85076667; PubMed=6510420;
MELZ-Boucigue M.-H., Jolles J., Marurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.,
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666 [1984].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sagripanti J.L.; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                             An 88 amino acid long C-terminal sequence of human
             TISSUE-Mammary gland;
MEDLINE-90326549; PubMed=2374734;
Powall M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013 (1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 670:243-254(1981).
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MEDLINE=99190892; PubMed=10089347;
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                                                                                                                                                                                                                                                                                                          SEQUENCE OF 609-711.
MEDLINE=82262043; PubMed=7049727;
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?EBS Lett. 142:107-110(1982).
  SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                             Camelus dromedarius (Dromedary) (Arabian camel)..
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus
NCBI_TaxID=9838;
                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRENE-Lactating mammary gland; STRAIN-Somall; TISSUE-Lactating mammary gland; Kappeler S.R.; Ackermann M., Farah Z., Puhan Z.; "Sequence analysis of camel (Camelus dromedarius) lactoferrin."; Int. Dairy J. 9:481-486(1999).
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BRNBL; AF165879; AAF82241.1; -.
HSSP; O77811; IBLX.
InterPro; IPRO1156; Transferrin.
PFdm; PRO405; transferrin; 2.
PRINTS; PRO4054; TR FER, 2.
PROSTTE; PSO2069; TRANSFERRIN.
PROSTTE; PSO206; TRANSFERRIN 1; 2.
PROSTTE; PSO206; TRANSFERRIN 3; 2.
PROSTTE; PSO206; TRANSFERRIN 3; 2.
PROSTTE; PSO207; TRANSFERRIN 3; 2.
PROSTTE; PSO207; TRANSFERRIN 3; 2.
         Score 61; DB 1; Length 711;
Pred. No. 0.0015;
1; Mismatches 1; Indels
                                                                                                             TRFL CAMDR STANDARD; PRT; 708 AA. O9TUÑO; 09M255; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
STRAIN=B1992816. PubMed=11997336;
Bao O, Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700 (2002).
-i- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                 15-UN-2002 (Rel. 41, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
508 ribosomal protein L28.
RPMB OR TTE1495.
Parkermoanaerobacter tengcongensis.
Bacteria; Firmidutes; Clostridia; Thermoanaerobacteriaceae; Thermoanaerobacteriaceae; Thermoanaerobacteriaceae; Thermoanaerobacterial L19072;
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Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
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-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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57.1%; Score 40; DB 1; Length 62; 77.8%; Pred. No. 0.81; ive 1; Mismatches 1; Indels

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SEGRETA TO 7343 / KID;
MEDLINE=96059641; PubMed=7476192;
BOTK P., Ouzounis C., Casari G., Schneider R., Sander C.,
Bolan M., Gilbert W., Gillevet P.M.;
"Exploring the Mycoplasma captricolum genome: a minimal cell reveals its physiology.";
Mol. Microbiol. 16:955-967(1995).
-! SIMILARITY: BELONGS TO THE COF/YEHA/YIDA/YIGL (E.COLI) / YCSE/YXEH (B.SUBTILIS) FAMILY.
                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypotherical protein (Fragment)
Mycoplasma capricolum.
Bacteria; Firmicutes; Mollicutes; Entomoplasmatales; Entomoplasmataceae.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-1- FUNCTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-1- SUBDINIT: MONOMER.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                              InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; IRR00159; Hypothet_cof.
Pfam; PF00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
Hypothetical protein.
NOW_TER 267 267
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PDB; 1B7U; 02-FBB-99.
PDB; 1B7U; 02-FBB-99.
Interbro; 1PR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
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nes 7, Conservative
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Schaefer U., Rausch O., Bouwmeester T., Pieler T.;
"Sequence-specific recognition of a repetitive DNA element by a C2H2
zainc-finger protein in Xenopus.";
Eur. J. Biochem. 226:567-576(1994).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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Pred. No. 9.9;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Gastrula zinc finger protein XFG20-1 (XLCGF20.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu Y., Teng C.T.;
"Chazacterization of estrogen-responsive mouse lactoferrin promoter.";
"Chazacterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885 (1991).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND THO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USFULLY BICARBONATE.
-!- SUBUNIT: MONOMER LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
Pentecost B.T., Teng C.T.;
Lactocranaferrin is the major estrogen inducible protein of mouse
uterine secretions ";
J. Biol. Chem. 262:10134-10139(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSBY, P02788, 1CBE.
MGD; MGI:96837, Ltf.
InterPort, Irgnolls6; Transferrin.
Pfam; PF03405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN. 1; 1.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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LACTOTRANSFERRIN
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SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
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Submitted (NOV-1996)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                 WEDLINE=90040698; PubMed=2599712;
Nietfeld W., El-Baradi T., Mentzel H., Pieler T., Koester M.,
Poeting A., Knoechel W.;
                                                                                                            Poeting A., Knoechel W., "Second-order repeats in Xenopus laevis finger proteins."; J. Mol. Biol. 208:639-659(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X82643; CAA57965.1; -.
PIR; S06565; S06565.
HSSP, P08046; 1AII.
TRANSPCT, T02366; -.
InterPro; IPR00822; Znf C2H2.
Pfam; PR00096; zf-C2H2; l8.
PRINTS; PR00048; ZINCTRIGER.
Probon; PR00003; Znf C2H2; 5.
SWART; SW00355; Znf C2H2; 18.
PROSITE; PS00028; ZINC_FINGER_C2H2 1; 17.
PROSITE; PS0157; ZINC_FINGER_C2H2 1; 17.
PROSITE; PS0157; ZINC_FINGER_C2H2 1; 17.
Zinc_finger; Metal-binding; DNA.binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70590; Q61799; Q922P2; C1-4NG-1988 (Rel. 08, Created) STANDARD (Rel. 11, Last sequence update) ST-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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TISSUE-Uterus;
MEDLINE-87280033; PubMed=3611056;
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                             85-613 FROM N.A.
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les 6; Conserv
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X. MEDLINE=92075758; PubMed=1742360;
X. Kruft V., Kapp U., Wittmann-Liebold B.;
X. Taracterization and primary structure of proteins L28, L33 and L34
T. The Bacillus stearchharmophilus ribosomes.";
Elsochimie 73:855-860(1991).
C. !- SIMILARITY: BELCONGS TO THE L28P FAMILY OF RIBOSOWAL PROTEINS.
R. PIR, A48395, A48395, A8390, R1bosomal L28.
R. InterPro; IPRO1383; Ribosomal L28.
R. TIGRAMS; TIGRO0009; L28; I.
R. RIBOSOWAL PIGRONS I.28; I.
R. RIBOSOWAL PROFESS I.
R. TIGRAMS; TIGRO0009; L28; I.
TIGRAMS; TIGRO0009; L28; I.
TINIT MET

O SEQUENCE 60 AA; 6810 MW; ZAD9161CD60B82F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
MJA RNR-1 INTEIN (POTENTIAL).
HYPOTHETICAL PROTEIN MJ0832, 2ND PART (POTENTIAL).
MJA RNR-2 INTEIN (POTENTIAL).
HYPOTHETICAL PROTEIN MJ0832, 3RD PART
                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN MJ0832, 1ST PART
                                InterPro; IRR03586; Hedgehog hintc.
InterPro; IRR03587; Hedgehog_hintc.
InterPro; IRR002203; Intein.
InterPro; IRR04402; Intein.
InterPro; IRR04402; Intein.
PF03477; ATP-cone; 2.
PRINTS; PR00379; INTEIN.
SWART; SW00306; Hintc; 2.
SWART; SW00306; Hintc; 2.
PROSITE; PS50818; INTEIN C TER; 2.
PROSITE; PS50819; INTEIN N TER; 2.
PROSITE; PS60819; INTEIN N TER; 2.
Hypothetical protein; Autocatalytic cleavage; Protein splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB 1; Length 1750;
Pred. No. 39;
3; Mismatches 2; Indels
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Pred. No. 1.8;
2; Mismatches 1; Indels
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Bacteria; Firmicutes; Bacillales; Geobacillus.
NCBI_TaxID=1422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
50S_ribosomal protein L28.
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54.5%;
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Best Local Similarity 54.5
---nes 6; Conservative
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1750
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RICS BACST
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P23374;
DT 01-NOV-1991
DT 16-OCT-2001
DE SOS TIDOSOMA
GN BACILLUS STO.
CC BACILLUS STO.
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CC PIR; A443395;
CC PIR; A443395;
CC PIR; A443395;
CC PIR; A43395;
CR FIRESPOSMA; TIL
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RL28 LISMO
ID RL28 LISMO
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              DR KWW WELL THE THE
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=868807;

MEDLINE=96337999; PubMed=868807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Rerlavage A.R., Dougherty B.A., Tomb-J.F., Adams M.D., Racho C.D., Rerlavage A.R., Dougherty B.A., Tomb-J.F., Adams M.D., Racho C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Feterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodoysky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
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Y832 METJA
ID Y832-METJA STANDARD; PRT; 1750 AA.
AC Q58242;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0832 (Contains: Mja rnr-2 DE intein].
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
ALINED (GLCNAC. ..) (POTENTIAL).
N-LINED (GLCNAC. ..) (POTENTIAL).
M-LINED (GLCNAC. ..) (POTENTIAL).
M-LINED (GLCNAC. ..) (FOTENTIAL).
M-> IQG (IN REF. 1).
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B-> G (IN REF. 2).
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Pred. No. 15;
1; Mismatches 4; Indels
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Archaea; Buryarchaeota; Methanococci; Methanococales;
Methanocaldococaceae; Methanocaldococcus.
NCBI_TaxID=2190;
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Best Local Similarity 54.5%;
Matches 6; Conservative 1
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HSSP; P17255; 1DFA.
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382
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707 AA;
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CONFLICT
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                                                                                                                                                                                                                                                               MEDLINE-21385309; PubMed=11493673;
Lee S.E., Jansen S., Frenz L.M., Johnson A.L., Fesquet D.,
Johnston L.H.:
"The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
                                                                                                                                                                                                                                                                                                                                                                        J. Cell Sci. 114:2345-2354(2001).
-!- FUNCTION: Part of a checkpoint which monitors spindle integrity and prevents premature exit from mitosis. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFAI/BUB2
MEDLINE=91330299; PubMed=1651171;
Hoyt M.A., Totis L., Roberts B.T.;
S. Cerevisiae genes required for cell cycle arrest in response to
loss of microtubule function.";
Cell 66:507-517(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Madrid E;
STRAIN=Madrid E;
BEDLINE-2990139499; PubMed=9823893;
Andersson S.G., Zonorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 306;
Pred. No. 15;
2; Mismatches 3; Indels
                                                                                                                                  SEQUENCE FROM N.A.
STRALM-S288C / AB972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00164; TBC; 1.
Cell cycle; Mitosis.
SEQUENCE 306 AA; 35027 MW; AIDDBFB548E81EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 39, Last sequence update)
ADP,ATP carrier protein 5 (ADP/ATP translocase 5)
Ricks or ILGS OR RP739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A39654; A39654.
SGD; S0004659; BUB2.
InterPro; IPR000195; RabGAP_TBC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last seq.
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M64706; AAA16885.1; -. EMBL; Z49703; CAA89765.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%;
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Best Local Similarity 50.v
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00566; TBC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia prowazekij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 CFAWQTQQRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFAWKRNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLCE RICPR
005962;
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TLCE RICPR
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                                                                                                                                                                                                                                                                                                                            Glaser P., Frangel L., Blocker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Warquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
"Comparative genomics of Listeria species.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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Pred. No. 1.9;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                         CLIP 11262 / Serovar 6a;
                                                                                                                                                                       Bacteria; Firmicutes, Bacillales, Listeriaceae, Listeria.
NCBL_TaxID=1639, 1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA43DE039213C562 CRC64;
                           5-JUN-2002 (Rel. 41, Created)
5-JUN-2002 (Rel. 41, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 306 AA.
                                                                                                                                                                                                                                                                    SPECIES=L.monocytogenes, and L.innocua;
STRAIN=EGD-e / Serovar 1/2a, and CLIP 1
MEDLINE=21537279; PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00830, Ribosomal_L28, I.
TIGRFRAMS, TIGR00009, L28, 1.
Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 6991 MW; AA43DE03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listilist, LIN01930, -.
Listilist, LMO01816; -.
InterPro, IPR001383; Ribosomal L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL591981; CAC99894.1; -. EMBL; AL596170; CAC97160.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.3%;
                                                                                                                                         Listeria monocytogenes, and
                                                                                             SOS ribosomal protein L28. RPMB OR LMO1816 OR LIN1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                Listeria innocua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4932;
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REAL SOC OS SEPTIONS SERVING S

RESULT 12 BUB2 YEAST

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Best Loca Matches

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human group B rotavirus ADRV.";
-/ Virol. '67:2730-2738(1931).
-/- SUBCELLULAR LOCATION: Outer capsid.
-/- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                        N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GLCNAC. N-LINEED (GL
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                                                                                                                                                                                                                                     EMBL; M91434; AAA47338.1; -.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84362 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.v.,
Best Local 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     133
407
527
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Shigella flexneri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFAWKRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                749 AA;
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                                                                                                                                                                                                                                                                                                                 Coat protein;
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CARBOHYD
SEQUENCE
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                                                                                                                      Andersson J.O., Andersson S.G.E.;
"Genomic rearrangements during evolution of the obligate
intracellular parasite Rickettsia prowazekii as inferred from an
analysis of 52015 bp nucleotide sequence.";
Microbiology 143:2783-2795(1997).
-!- FUNCTION: PROVIDES THE RICKETTSIAL CELL WITH HOST ATP IN
EXCHANGE FOR RICKETTSIAL ADP. THIS IS AN OBLIGATE EXCHANGE SYSTEM.
THIS ENERGY ACQUIRING ACTIVITY IS AN IMPORTANT COMPONENT OF
RICKETTSIAL PARASITISM (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ADP/ATP TRANSLOCASE TLC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=93233240; PubMed=8386274;
Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.;
"Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VP4 ROTGA STANDARD, PRT; 749 AA.

004916;

01-JUN-1994 (Rel. 29, Created)

01-JUN-1994 (Rel. 29, Last sequence update)

01-JUN-1994 (Rel. 29, Last annotation update)

outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
Virus_TaxiD=12705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.9%; Score 37; DB 1; Length 500; 54.5%; Pred. No. 25; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane, Transport, ATP-binding, Multigene family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FE3DB48D08CF5F72 CRC64;
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                                                                                                          MEDLINE=97419517; PubMed=9274032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, Y11778; CAA72457.1; -.
InterPro; IPR004667; ADP_ATP_car.
Pfam; PF03219; TLC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ235273; CAA15167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57073 MW;
                                                                    SEQUENCE OF 325-500 FROM N.A. STRAIN=Madrid E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGREAMS; TIGRO0769; AAA; 1.
                                    Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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1114
2204
2244
307
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500 AA;
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Best Local Similarity
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TRANSMEM 26
TRANSMEM 62
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TRANSMEM
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation-the Buropean Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21534947; PubMed=11677608;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J. Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebainia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Larsen T.S., Lacther B., Mule S., O'Gaora P., Parry C., Marchead S., Barrell B.G.;
Mitchead S., Barrell B.G.;
Wintehead S., Barrell B.G.;
Wintehead S., Barrell B.G.;
Wintehead S., Rarell B.G.;
Wintehead S., Parry C., Whitehead S., Parry C., 
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SEPCISS-S.-E. Laxmerti,
MEDLINE-85014891; PubMed-6091128;
Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pHCM1, and Plasmid IncFII NR1.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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(POTENTIAL)
(POTENTIAL)
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20-WAR-1987 (Rel. 04, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Mercuric transport protein (Mercury ion transport protein)
MERT OR HCM1.234C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB 1; Length 749; Pred. No. 38;
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                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Integral membrane protein, Inner membrane.
Haberstroh L., Silver S.;
"Mercuric ion-resistance operons of plasmid R100 and transposon infol. the beginning of the operon including the regulatory region and the first two structural genes.";
Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
                                                                                                                                                                                                                          Jasamid NRI.";
7. Mol. Appl. Genet. 2:601-619(1984).
:!- PUNCTION: INVOLVED IN MERCHRIC TRANSPORT. PASSES A HG(2+) ION
FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE
                                                                                                                        PRICIES ILEXARI; PLASMID-INCFII NRI; TRANSPOSON-TN21;
MEDLINE-85159407; PubMed-6530603;
Sarrineau P., Gilbert P., Jackson W.J., Jones C.S., Summers A.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fam; PF02411; MerT; 1. ransport; Mercury; Plasmid;
                                                                                                                                                                                isdom S., The DNA sequence of the mercury resistance operon of the IncFII _{\mbox{\scriptsize The}}
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Pred. No. 8.3;
1; Mismatches 3; Indels
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HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
HG(2+) (POTENTIAL).
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InterPro; IPR003457; Transprt_MerT.
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12521 MW;
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EMBL; J01730; AAA92261.1; -.
EMBL; K03089; AAB59075.1; -.
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Best Local Similarity 63.6%;
Matches 7; Conservative
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116 AA;
                                                                                                           SEQUENCE FROM N.A.
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TRANSMEM 16
TRANSMEM 46
                                                                                                                                                                                                                      plasmid NR1
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SEQUENCE
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Search completed: February 21, 2003, 07:51:41 Job time : 6.2093 secs

FAWKRNMRKVR 12

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64 FAWKRIYRPVQ 74

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Gaps

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Q92rh8 rhizobium m Q97k18 rhizobium m Q97k1 brucella me Q83112 rattus norv Q931780 caenorhabdi Q92k19 musculu Q92k4 helicobacte O1749 caenorhabdi P9383 arabidopsis Q91217 homo sapien Q91k6 homo sapien Q91k6 homo sapien Q9683 human immun Q9883 quillardia Q92x1 quillardia Q92x1 quillardia Q94x1 qerobacteri Q94x1 qerobacteri Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q954x1 qerosphila Q956x1 arabidopsis Q966x2 homo sapien Q956x2 arabidopsis Q966x1 hm capien Q956x1 hm capien Q956x1 rhizobium l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2010 (TrEMBLrel. 17, Last annotation update)
Lactoferrin honolog (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 80.0%; Score 56; DB 4; Length 711; Best Local Similarity 81.8%; Pred. No. 0.1; Matches 9; Conservative 1; Mismatches 1; Indels
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TISSUE-PROSTATE;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -.
SEQUENCE 711 AA; 78327 MW; 1B9C7EB097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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                    Q92RH8
Q8YFK3
Q63112
Q93780
Q98Q19
Q8RZA4
Q9ZRZA4
Q17549
P93833
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Q9UFK6
Q9CA22
O90863
Q98RR2
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Q95K05
Q96GY3
Q9C6N2
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Q9ADZ8
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Q9UCY5;
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Q9UCYS
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Q8TCD2
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Ogz462 salmonella
O25611 helicobacte
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                                                                         2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Q9UCY5
Q25411
Q9T810
Q9UZ5
Q9HPA3
Q9HPA3
Q9R9U1
Q8R9U1
Q9BXW1
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09PQS6
063104
Q8U6K3
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
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sp_phage:*
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sp_bacteria:*
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sp_human:*
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sp_plant:*
sp_rodent:*
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065237 arabidopsis

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Gaps

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Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
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TIGR; HP0957; -
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
Lactoferrin (Fragment).
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Matches 5; Conservative
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Matches 5, Conserv
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                                                              NCBI_TaxID=210;
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01-OCT-2000 (
01-JUN-2002 (
                                                                                                                                                                                                                                                                                                                                   Venter J.C.;
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ID 09443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Feltwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella Marrice Allega Serovar Tybhi CI18.";
                                                                                                            Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 4.4;
0; Mismatches 4; Indels
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 74.3%; Score 52; DB 4; Length 38; ilarity 81.8%; Pred. No. 0.026; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ll protein; Complete proteome.
511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                         Interpro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 AA
                                                                                                                                                                     Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
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                                                                 SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:848-852(2001).
EMBL; AL627276; CAD06049.1; -.
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Best Local Similarity 66.7%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          2 FAWKRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                 21 FOWORINMRKVR 31
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                                                                                                                                                 seminal plasma."
                            NCBI_TaxID=9606;
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SEQUENCE 51
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Q8Z462

Q8Z462

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RESULT 4 025611

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SEQUENCE FROM N.A.
STRAIN=26655 / ArCC 700392;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9252185;
MEDLINE=97394467; PubMed=9787;
MEDLINE=97394467; PubMed=9787;
MEDLINE=97394467; PubMed=9787;
MEDLINE=97394467; MEDLINE=9787;
MEDLINE=9789 M., FutzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
METGROEN M., Methman J.M., Futit C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gastric pathogen Helicobacter \mathbf{pylori.}^{n},
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
NCDI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 6%; Score 41; DB 6; Length 33; ilarity 45.5%; Pred. No. 2; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein, Transferase, Complete proteome. SEQUENCE 393 AA, 45622 MW; 6428BA3321554F46 CRC64;
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Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
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InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
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445 CFTWRKDMERKR 456
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Best Local Similarity
Matches 5; Conserv
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Matches 7; Conserv
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Q8R9U1
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Q9BXW1
                       SKRRRRS
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MEDILINE=20504483; PubMed=11016950;
MGDILINE=20504483; PubMed=11016950;
MGDILINE=20504483; PubMed=11016950;
MGDILINE=20504483; PubMed=110.
MGDILINE=20504483; MGDILINE A., Thorsson V., Sbrogna J., Swartzell S., Mellor D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H. Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20241927; PubMed=10777661;
Buchner G., Orfanelli U., Quaderi N., Bassi M.T., Andolfi G.;
Buchner G., Orfanelli U., Quaderi N., Bassi M.T., Andolfi G.;
Buchner G., Orf a new EGF-repeat-containing gene from human Xp22:
Acandidate for developmental disorders.";
Genomics 65:16-23(2000)
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Hypothetical 61.5 kDa protein.
EGFL6 OR W80.
Was musculus (Mouse).
Eukar myczylus (Acazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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PROSITE; PS00012; EGF_1; UNKNOWN_1.
PROSITE; PS00186; EGF_2; 2.
PROSITE; PS01187; EGF C2; 2.
PROSITE; PS50060; MAM_2; 1.
Calcium-binding; EGF-1; Ke domain; Glycoprotein; Hydroxylation; EGPCLA: 550 AA; 61520 MW; DEF936325C9F31B3 CRC64;
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Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                Franco B.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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Archaea, Buryarchaecta, Halobacteria, Halobacteriales,
Halobacteriaceae, Halobacterium.
NCBI_TaxID=64091;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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-!- SMILARITY: CONTAINS 1 MAM DOWAIN
EMBL; AJZ45672; CAB92138.1; -.
HSSP; P35555; 1EMN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000561; EGF-like.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR000998; MAM_domain.
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MART; SM0001; EGF_like; 2.
MART; SM00137; MAM; 1.
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fam; PF00629; MAM;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Thermoanaerobacter tengcongensis.
Bacteria; Firmfcutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBI_TaxID=119072;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z., Lu F.,
Yu W.-Q., Sun B.-Z., Chai Y.-B., Zhu F., Liu X.-S., Li Z., Lu F.,
Yan W., Yang H., Zhao Z.-L.;
"Human acute promyelocytic leukemia cell line NB4's
apoptosis/diferentiation related genes.";
submitted (JUT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AR277183; AAKO7542.1;
InterPro; IPR000717; PCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

BMBL, ARD13107; AAM24713.1; -.

Complete proteome.

SEQUENCE 62 AA, 7037 NW; CAADB605C81D495D CRC64;
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                                                                                                                                                                                                                                                        58.6%; Score 41; DB 17; Length 584;
41.7%; Pred. No. 39;
ative 4; Mismatches 3; Indels
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                                                                                                                                                                                                  584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005078; AAG19967.1; -.
InterPro; IPR001646; Speptide repeat.
InterPro; IPR001622; K+channel_pore.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Ribosomal protein L28.
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01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
PNAS-125.
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SEQUENCE PROM N.A.

STRAIN=MAT / JCM11007,

MEDLINE=21992816; PubMed=11997336;
                                                                                                                       Pfam; PF00805; Pentapeptide; 2. Complete proteome. SEQUENCE 584 AA; 65151 MW; 2
                                                                                                                                                                                                                                                                                                                               5; Conservative
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01-UJN-2001 (TrEMBLrel. 17, Created)
01-UJN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to dendritic cell protein.
Similar to dendritic cell protein.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                               Homo papiens (Human),

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTC-2002 (TrEMBLrel. 21, Last annotation update)
DJ69B10.1 (GA17 protein) (Hypothetical 42.5 kDa protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strauberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL078477; CAC68392.1; -.
InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
Hypothetical protein.
SEQUENCE 374 Aa; 42503 MW; 63736CA2B093D794 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cobley V.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Matches 6, Conservative
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3 AWKRNMRKVR 12
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Q96KM8
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Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;

"Identification of G protein-coupled receptor genes from the human genome sequence.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB083609; BAB89322.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                     57.1%; Score 40; DB 4; Length 206; 60.0%; Pred. No. 20; cive 3; Mismatches 1; Indels
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Zhao Z., Husng X., Li N., Zhu X., Cao X.;
"A novel gene from human dendritic cell.";
Submitted (Max-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFF064603; AAC17108.1; -.
InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SMO088; PINT; 1.
SEQUENCE 374 AA; 42512 MW; 2CFF2BCB70F997A7 CRC64;
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
SEQUENCE 206 AA; 23754 MW; 940D5B66271A44B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AA; 33557 MW; AB7F9792957BFCA6 CRC64;
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01.AUG-1998 (TrEMBLrel. 07, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative G-protein coupled receptor.
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Best Local Similarity 60.0-
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Best Local Similarity 100.4
Matches 6; Conservative
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Homo sapiens (Human)
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|72 AWKQNLNKVK 181
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TISSUE=BLOOD;
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SEQUENCE
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STRAIN=BD II; TISSUB-LIVER;
MEDLINE=89214106; PubMed=2708349;
Kodelja V., Lucas K., Barnert S., von Kleist S., Thompson J.A.,
Zimmermann W.A.;
"Identification of a carcinoembryonic antigen gene family in the rat:
"Identification of the N-terminal domains reveals immunoglobulin-like,
hypervariable regions.";
J. Biol. Chem. 264:6906-6912(1989).

EMBL:
M60026; AAA40911.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116,
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MEDLINE=20500219; PubMed=11048724;
Glass J.I., Lefkowitz B.J., Glass J.S., Heiner C.R., Chen E.Y.,
Cassell G.H.;
"The complete sequence of the mucosal pathogen Ureaplasma
urealyticum.";
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                                                                                                                                                                                                                                 Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria, Firmicutes, Bacillus/Clostridium group, Mollicutes,
Wycoplasmatacae, Ureaplasma.
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PROSITE, PS10011, PROTEIN KIRASE DOM; 1.
PROSITE; PS01016, PROTEIN KIRASE ST, UNKNOWN 1.
PROSITE, PS010106, PROTEIN KIRASE_ST, UNKNOWN 1.
SEQUENCE 386 AA; 45241 MW; 789374CC15D1CAD9 CRC64;
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                                               Q9PQS6 PRELIMINARY; PRT; 386 AA. Q9PQS6, O1-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) PKN OR U0216.
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Nature 407.757-762(2000).
Nature 407.757-762(2000).
EMBL; AE002120, AAR30624.1; -.
InterPro; IPR00019; Euk pkinase.
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                        February 21, 2003, 07:37:21 ; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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		·	AAR44841 Lactoferrin-relate AAR4853 Lactoferrin derive AAR5854 Lactoferrin derive AAR57461 Lactoferrin derive AAR57462 Lactoferrin derive AAR84698 Bovine lactoferrin AAR84659 Anti-parasitic lac AAR80264 Anti-parasitic lac AAR80265 Anti-parasitic lac AAR80265 Anti-parasitic lac AAR80565 Lactoferrin AAR91852 Lactoferrin-derive AAR91862 Lactoferrin-derive	ALIGNMENTS AA. ide SEQ ID NO:95. on; infection; inflammation; tumour; lammatory; anti-tumour; is; Candida infection; fungicidal; is; Candida Lifection; fungicidal; Baltzer L, Dolphin GT;
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                                                              AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fundicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
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                                                                                                                                                                            anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                              0; Gaps
          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                           Claim 22; Page 38; 102pp; English.
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98SE-0002562.
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infections a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.00038;
0, Mismatches 1; Indels
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29-DEC-1998;
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12 AA;

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Sequence
                                          Query Match
                                                                    Matches
                                                                                                                                                         RESULT 5
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ID AAY
     X 8
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                                                                                                                                                                                                AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through lactoferin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment or no be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumnoural properties they cannot be used clinically on a bytoid basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                            Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                              Score 62; DB 21; Length 12;
Pred. No. 0.00057;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:89.
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                                                                                                                                                                                                                                                                         AAY78089 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 22; Page 37; 102pp; English
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                                                                                                                               91.2%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98SE-0002441.
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                                                                                                                                                                                                                                                                                                                                                                                                                     bactericidal; preservative
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                       11; Conservative
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                                                                                                                                                                                 1 CFAWQRAMRKVR 12
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                                                                                                                            Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                       12 AA;
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29-DEC-1998;
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                                                                                                       Seguence
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as curinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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Score 59; DB 21; Length 12;
Pred. No. 0.0018;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       th 86.8%; Score 59; DB 21; Length 12; Similarity 83.3%; Pred. No. 0.0018; 10; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:90.
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                                                                                                                                                                                                                                                                                                                                 AAY78090 standard; Peptide; 12
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86.8%;
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                                                             10; Conservative
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                                                                                                                       1 CFAWQRAMRKVR 12
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                                   Local Similarity
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Best Local Similarity
Matches 10; Conserv
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17-JUL-1998;
29-DEC-1998;
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RESULT 6

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactucidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                          food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal; bactericidal; preservative.
                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:86.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 36; 102pp; English.
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AAY78086 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                  (first entry)
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nes 10; Conservative
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17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                      Homo sapiens.
Synthetic.
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                                                                                     25-APR-2000
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                                          AAY78086;
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Matches
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                                                                                                                                                                                                                                                                                                                                                 food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 21; Length 12;
Pred. No. 0.0018;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:93.
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                                                                                                                                                AAY78093 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3%;
Matches 10; Conservative
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17-JUL-1998;
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Dolphin GT;

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Human lactoferrin derived peptide SEQ ID NO:94,

25-APR-2000 (first entry)

RESULT 7 AAY78086

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Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

98SE-0002441. 99WO-SE01230.

98SE-0004614

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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                 Claim 12; Page 70; 102pp; English.
                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
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                         WO200001730-A1
                                                                    06-JUL-1999;
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 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                 lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fundicidal and bactericidal and may also be used a preservatives. Even though native human lactoferrin have been shown to have desired
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          Human, lactoferrin, modification; infection, inflammation; tumour;
food, infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                 Dolphin GT;
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                                                                                                                                                                                                                                                 Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                 Claim 22; Page 38; 102pp; English.
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                                                                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.3%;
                                                                                                                                                    99WO-SE01230,
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                         (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFAWORAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFAWKRNMRKVR 12
                                                                                                                                                                                                                                                                      WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 AA;
                                                                                                     WO200001730-A1.
                                                                                                                                                                         06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                    sapiens
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                                                                                                                                                   06-JUL-1999;
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                                                                                                                           13-JAN-2000
                                                                                Synthetic
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                                                                    Homo
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AAY78038
AAY78038
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as urinary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57; DB 21; Length 12; Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78046 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.8%;
83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFAWORAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AA;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment or an eased for treating and/or prevention of infections (such as urinary tract infections. Collisis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as triffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 21; Length 12;
Pred. No. 0.0039;
0; Mismatches 2; Indels
                                                                                                         Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lactoferrin derived peptide SEQ ID NO:47.
                                                                                                         Baltzer L,
                                                                                                                                                                                                                  Claim 15; Page 35; 102pp; English.
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                                                                                                         Hanson LA, Mattsby-Baltzer I,
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           98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                          (ASCI-) A+ SCI INVEST AB
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17-JUL-1998;
29-DEC-1998;
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                                          29-DEC-1998;
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           06-JUL-1998;
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AAY78047
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferin. The peptides are taken up in the intestine through binding to specific lactoferin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as curinary tract infections, collitis, and Candida infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungloidal and bactericidal and may also be used as preservatives. Even though native human lactoferin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                               83.8%; Score 57; DB 21; Length 12; 83.3%; Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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 Dolphin GT
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Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78037 standard; Peptide; 13 AA.
                                                                                                              Claim 18; Page 73; 102pp; English
 Hanson LA, Mattsby-Baltzer I,
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98SE-0002562.
98SE-0004614.
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les 10; Conservative
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                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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29-DEC-1998;
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urinary tract infections, colitis, and Candida infection on a mucosal
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                                               AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or prevention of infections on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Been though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used all inically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
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Claim 12; Page 70; 102pp; English
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17-JUL-1998;
29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as unembrane), inflammations and/or tumours. The peptides can also be used in food sulfs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungloidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57; DB 21; Length 13;
Pred. No. 0.0042;
0; Mismatches 2; Indels
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Best Local Similarity 83.3
Matches 10; Conservative
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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98SE-0002562.
98SE-0004614.
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Best Local Similarity 83.3%;
Matches 10; Conservative
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29-DEC-1998;
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Length 14;

83.8%; Score 57; DB 21;

Query Match

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Pred. No. 0.0045;
0; Mismatches 2;
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                      83.3%;
                    Best Local Similarity 83.3
Matches 10; Conservative
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.
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APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, SHIGEAKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: TANAKA, SHON'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: OF INVENTION: INHIBITORS
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INVENTION: INHIBITORS
OCREESPONDENCE ADDRESS:
ADDRESSEE: PATERY ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBRAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/204,487
FILING DATE: O2-MAR-1994
CLASSIFICATION NUMBER: 134
ATTONARY/AGENT INPORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFRENCE/DOCKET NUMBER: 32,503
TELEPRANCE/DOCKET NUMBER: FJN-019
TELEPRANCE/DOCKET NUMBER: 617) 248-7100
TELEPRANCE (617) 248-7100
TELEPRANCE (617) 248-7100
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FURTHER. 18 AMINO ACIGS
                                    US-08-724-586-2
US-09-421-632-2
US-08-655-640-2
US-08-655-640-4
US-08-154-019-4
US-08-461-133-4
US-08-461-167-4
US-08-464-167-4
US-08-464-167-4
US-08-441-67-4
US-08-441-67-4
US-08-476-798-4
US-08-476-798-4
US-08-476-798-4
US-08-456-681-2
US-08-250-308-2
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US-08-456-108-2
US-09-265-577-2
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Patent No. 5565425
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STRANDEDNESS: single
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MOLECULE TYPE: peptide
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COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-08-204-487-3
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 6
Sequence 6
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Sequence
Sequence
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/cgn2 6/ptodate3/liaa/5A_COMB.pep:*
/cgn2 6/ptodate3/liaa/5B_COMB.pep:*
/cgn2 6/ptodate3/l/iaa/6A_COMB.pep:*
/cgn2 6/ptodate3/l/iaa/6B_COMB.pep:*
/cgn2 6/ptodate3/l/iaa/PcTUS_COMB.pep:*
/cgn2 6/ptodate3/l/iaa/PcTUS_COMB.pep:*
/cgn2 6/ptodate3/l/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-09-508-734-4
3-09-508-734-6
3-07-755-161A-10
3-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5-161A-3
                                                                                                                                                                                                                                                                                                                                                               262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                   US-09-743-107B-95
68
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Match Length
                                                                                                                                       February 21,
                                    Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                           score:
                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                                                                     Title:
Perfect
                                                                                                                                       Run on:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
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Best Local Similarity 83.3
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                         STREET: 411 Hacken
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFAWORAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
US-08-475-055-8
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                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YONG MING LI
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ADPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                               Gaps
                                                                                                                                               ö
                                                                                                  Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.8%; Score 57; DB 2; Length 18; Best Local Similarity 83.3%; Pred. No. 0.0016; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                             Score 57; DB 1;
Pred. No. 0.0016;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFCATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
APPLICATION NUMBER: 08/418,642
FILING DATE: 4PRL 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NUMBE: Jackson Eq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELEPHONE: 20,1487-5600
TELEPHONE: 20,1487-5600
TELEFAX: 20,1343-164
TELEFAX: 20,1343-164
TELEFAX: 20,343-166
TELEFAX: 20,343-166
TELEFAX: 20,0487-5600
TELEFAX: 20,0487-5600
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TELEFAX: 20,0487-5600
                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08485948
Patent No. 5855882
GENERAL INFORMATION:
;
US-08-204-487-3
                                                                                             Query Match 83.8%;
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                        1 CFAWORAMRKVR 12
                                                                                                                                                                                                                                     1 CFOWORNMRKVR 12
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1 CFAWQRAMRKVR 12

1 CFOWORNMRKVR 12

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SECURE NO. 5051341

GENERAL INFORMATION:

APPLICANT: UL. YONG MING
APPLICANT: UL. YONG MING
APPLICANT: UL. YONG MING
APPLICANT: UL. YONG MING
APPLICANT: UL. YONG MING
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APPLICANT: UL. YONG MING
APPLICANT: UL. YONG
INTER SECURE ALDERSE: A GOLGON
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INTER SECURE ALDERSE: A GOLGON
CONDUTE: MAY DECOMINE A GOLGON
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CONDUTE: A GOLGON
CONDUTE:
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us-09-743-107b-95.rai

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/note= "thiol group of
Cys residue at location 19 connected by disulfide bond with
thiol group of Cys residue at location 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEAVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                                                                                                                        NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEFAX: 202-371-8856
                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
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LOCATION: 19
LDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
                       DisplayWrite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: CH
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MARP POSITION:
UNITS:
FEATURE:
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DEVELOPMENTAL STAGE
        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
TISSUB TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07755161A
Fatent No. 5304633
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CONTRICT WASHINGTON
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRAL APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 57; DB 2;
Pred. No. 0.0016;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
CLASSIFICATION: MARER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/ABRIT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 947-1-(
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELEPRANCHICATION INFORMATION:
TELERA: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
                                                          Hackensack
: New Jersey
tr: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFAWQRAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNWRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                                                              STATE: Ne COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-07-755-161A-3
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OTHER INFORMATION: "Disce= "thiol group of OTHER INFORMATION: "Instead of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"

REATURE:
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
COTHER INFORMATION: Once= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATARU
APPLICANT: TANAKA, SHICEAKI
APPLICANT: TANAKA, SHICEAKI
APPLICANT: TANAKA, SHICEAKI
APPLICANT: TANAKAKI, YOSHIHIRO
APPLICANT: TANABAKI, YOSHIHIRO
APPLICANT: UNIDA, TOSHIKI
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 57; DB 1; Length 20;
Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TEADABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT IN-PORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFRENCE/POCKET NUMBER: FJN-019
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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CITY: BOSTON
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FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
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Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YANAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.8%;
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Best Local Similarity 83.3
Matches 10; Conservative
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VOLUME:
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                                      Gaps
83.3%; Pred. No. 0.0017; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskettee, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTMARE: Displaymite
SOFTWARE: Displaymite
CURRENT APPLICATION DATA:
PILING DATE: 29-MAY-1992
CLASSIPICATION DATA:
PILING DATE: 29-MAY-1992
CLASSIPICATION DATA:
APPLICATION TO SEP-1991
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8856
TELEPHONE: 202-371-8856
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FEATURE:
NAME/KEY: modified site
Best Local Similarity 83.3
Matches 10; Conservative
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
CELL TYPE:
CELL LIVE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIMERY:
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CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                 1 CFAWORAMRKVR 12
                                                                                                                                                            2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                             RESULT 6
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1 CFAWQRAMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-08-381-984-24
    US-08-256-771-24
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Sequence 24, Application US/08256771

Patent No. 556591

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

ITILE OF INVENTION: PRODUCTS THEREWITH

TILLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
IDENTIFICATION METHOD:
OFFIRE INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                     NAME/KEY: Peptide
LOCATION: 1..20
OCHER INPORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OFBRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JULY 22, 1994
PRIOR APPLICATION 1514
PRIOR APPLICATION WHERE:
FILING DATE:
APPLICATION WHERE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                               LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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STRANDEDNESS: si
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18-08-256-771-25
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83.8%; Score 57; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.0017;
Matches 10; Conservative 0; Mismatches 2; Indels
Length 20,
                                                                                           2; Indels
    Score 57; DB 1;
Pred. No. 0.0017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
    Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TRNGTH: 20 aming acids
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MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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RESULT 12
US-09-508-734-4
; Sequence 4, Application US/09508734
; Sequence 4, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Samyang Genex Corporation
; TILE OF INVENTION: Useful microorganism thereof
; TILE OF INVENTION: Useful microorganism thereof
; FILE REFRENCE: PA/SYG/O0139
; CURRENT APPLICATION NUMBER: US/09/508,734
; CURRENT FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: KR1998-29351
; PRIOR FILING DATE: 1999-07-13
; RIOR FILING DATE: 1998-07-13
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment ther
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTHER INFORMATION: And 19 are chemically modified to prevent disulfide linkage US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.0017;
0; Mismatches 2; Indels
                                                                                                       COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
    STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIETRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 anino acids
TYPE: anino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFAWORAMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                          COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83.8%; Score 57; DB 1; Length 20;
83.3%; Pred. No. 0.0017;
live 0; Mismatches 2; Indels
                                                                                                                                                                                                                    COUNTRY: WASAILINGTON
STATE: WASAILINGTON
ZIP: 20005
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER: LIB COMPACTED STATE
COMPUTER: LIB COMPACTED STATE
COMPUTER: LIB COMPACTED STATE
COMPUTER: LIB COMPACTED STATE
COMPUTER: LIB COMPACTED STATE
COMPUTER: WORDPICTON DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: LISS
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REGERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
Sequence 24, Application US/08381984

Patent No. 5804555

GENERAL INFORMATION:
MURDEL OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORWATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFAWQRAMRKVR 12
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FEATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "thiol group of Cys residue at location 4 connected by disulfide bond with thiol group of Cys residue at location 21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-371-8850
TELEPAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol.
                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY: linear
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
POSTITION IN GENOME;
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
CELL LINE:
IMMEDIATE SOURCE:
LIBBARY:
                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-508-734-6
Squence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-14
PRIOR PRILING DATE: 1998-07-13
SOFTWARE: Kopatentin 1.71
SOFTWARE: Kopatentin 1.71
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                                                                                                             Query Match 83.8%; Score 57; DB 4; Length 22; Best Local Similarity 83.3%; Pred. No. 0.0019; Matches 10; Conservative 0; Mismatches 2; Indels
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WESULT 14

WESULT 16

Sequence 10, Application US/07755161A

Patent No. 5304633

Patent No. 5304633

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER RADDALE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500KD

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS.-DGS

SOFTWARE: DisplayWrite

CURRENT APPLICATION DATA:

APPLICATION UNBER: US/07/755,161A

FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-508-734-6
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                       1 CFAWORAMRKVR 12
                                                                                                                                                                                                                                                2 CFQWQRNMRKVR 13
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Gaps . 0

Indels

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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" PUTHORS: AUTHORS:
                                                                                                                                                                                                                                                                                   Score 57; DB 1; Length 25;
Pred. No. 0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 21, 2003, 08:04:27 Job time : 8.93023 secs
                                                                                                                                                                                                        FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                     83.8%;
83.3%;
                                                                                                                                                                                                                                                                                                  Best Local Similarity 83.3
Matches 10; Conservative
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                 4 CFQWQRNMRKVR 15
                                                                                                                                                                                        DOCUMENT NUMBER:
                                                                                        TITLE:
JOURNAL:
VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                     Query Match
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Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
                       Sequence 10, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: ZO005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                  modified site 21
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IDENTIFICATION METHOD:
OTHER INFORMATION: /not
OTHER INFORMATION: Cys
OTHER INFORMATION: thic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL IYPE:
CELL LINE:
CREANELLE:
IMMEDIATE SOURCE:
LIBRARY:
LIBRARY:
CLONE:
CLONE:
CROWNOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
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NAME/KEY:
LOCATION:
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us-09-743-107b-95.rapb

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APPLICANT: BALDUR SVEINBJ (RNSSON
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Sequence 2, App
Sequence 2, Appl
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                                                                                                                          February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Sequence 10,
Sequence 4884,
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Sequence 7, 7
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Sequence 30,
Sequence 14,
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:/
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/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:/
/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:/
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'ptodata/2/pubpa/USO6 PUBCOMB.pep:*
'ptodata/2/pubpa/USO7 PUBCOMB.pep:*
'ptodata/2/pubpaa/USO7 PUBCOMB.pep:*
'ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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                   GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-995-542-10
US-09-738-626-4884
US-10-080-960-11
US-09-948-078-2
US-09-888-320-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 todata/2/pubpaa/US08_
                                                                                                                                                                                                                                                                                                                                  156504 segs, 31069816 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                               US-09-743-107B-95
68
1 CFAWQRAMRKVR 12
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Maximum DB seq length: 200000000
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Match Length DB
                                                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                            Run on:
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34 50.0 46 10 US-09-864-761-35744 Sequence	1 34 50.0 209 10 US-09-904-536-9 Sequence 9, Appl 34 50.0 209 10 US-09-904-536-9 Sequence 9, Appl 4 34 50.0 209 10 US-09-904-536-11 Sequence 11, Appl 5 50.0 209 10 US-09-904-536-11 Sequence 12, Appl 5 50.0 209 10 US-09-904-536-13 Sequence 13, Appl 6 34 50.0 209 10 US-09-904-536-13 Sequence 13, Appl 6	34 50.0 209 10 US-09-904-536-14 Sequence 34 50.0 209 10 US-09-904-536-15 Sequence 34 50.0 209 10 US-09-904-536-16 Sequence 34 50.0 209 10 US-09-904-536-17 Sequence 34 50.0 209 10 US-09-904-536-18 Sequence 34 50.0 209 10 US-09-904-536-18	2 34 50.0 212 10 US-09-904-536-10 Sequence 3 34 50.0 235 9 US-10-095-449-6 Sequence 4 34 50.0 235 10 US-09-448-378-1 Sequence 5 34 50.0 235 10 US-09-488-378-1 Sequence	6 34 50.0 235 10 US-09-904-536-1 Sequence 7 34 50.0 365 9 US-10-109-533A-2 Sequence 8 34 50.0 372 9 US-09-764-868-1044 Sequence 9 34 50.0 1192 9 IIS-10-170-102-2 Sequence	1 33 48.5 67 9 US-09-796-692-1487 Sequence 1 33 48.5 81 10 US-09-864-761-41887 Sequence 2 33 48.5 171 10 US-09-764-864-1119 Sequence 3 33 48.5 171 10 US-09-764-864-1536 Sequence	4 33 48.5 579 10 US-09-824-588-z Sequence 2, Apr. 5 33 48.5 620 10 US-09-764-864-1116 Sequence 1116,	ALIGNMENTS	RESULT 1 US-09-798-869-2 Sequence 2, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION: APPLICANT: JOHN SIGTED SYRNDSEN APPLICANT: GYTZIN REKDAL TILLE APPLICANT: BALDUR SYRINBGINSON APPLICANT: BALDUR SYRINBGINSON TILLE REFERENCE: A34049-FCT-USA-A CURRENT PAPLICATION: DIAGNOTIVE PEPTIDES FILE REFERENCE: A34049-FCT-USA-A CURRENT FILING DATE: 2001-02-27 PRIOR PELICATION NUMBER: PCT/C899/02851 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-38 NUMBER OF SEQ ID NOS: 30 SOFFWARE: PRECED WINDOWS VERSION 4.0 SEQ ID NO 2	LENGTH: TYPE: PR ORGANISM 9-798-86	Query Match Best Local Similarity 83.3%; Pred. No. 0.00055; Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	OY 1 CFAWQRANRKVR 12 	RESULT 2 US-09-798-869-20 i Sequence 20, Application US/09798869 j Publication No. US20030022821A1 j GENERAL INFORMATION j APPLICANT: JOHN SIGNED SVENDSEN j APPLICANT: USEN REKEAN j APPLICANT: USEN REKEAN j APPLICANT: USEN REKEAN
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Gaps
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens
OTHER INFORMATION: sequence)
US-09-798-869-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                         ;
Score 57; DB 9; Length 694; Pred. No. 0.027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 49; DB 9;
Pred. No. 0.013;
                                       0; Mismatches
                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09798869
| Publication No. US20030022821A1
| GRNERAL INFORMATION:
| APPLICANT: USTBIN REXDAL
| APPLICANT: USTBIN REXDAL
| APPLICANT: LARS VORLAND
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| FILE REFERENCE: A34049-PCT-USA-A
| CURRENT APPLICATION NUMBER: US/09/798,869
| CURRENT PILING DATE: 2001-02-27
| PRIOR PILING DATE: 1999-08-31
| PRIOR FILING DATE: 1999-08-31
| PRIOR FILING DATE: 1999-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 30
SOFTWARE FRAISEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
83.8%;
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75.0%;
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ORGANISM: Artificial Sequence
                                       10; Conservative
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Best Local Similarity 75.0
Matches 9; Conservative
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                                                                            1 CFAWQRAMRKVR 12
                                                                                                              22 CFOWORNMRKVR 33
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 Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin COMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Pice, Holman & Stern
                                                                                                                                                                                                                                                                                                                   Ouery Match 83.8%; Score 57; DB 9; Length 25; Best Local Similarity 83.3%; Pred. No. 0.00093; Matches 10; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Jacobson, Price, Holman & Stern STEET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
                 TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PELING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREESEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REGISTRATION NUMBER: 31,409
TERERENCE/DOCKET NUMBER: 10505/P58185C
TELECHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
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Gaps . 0

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Mismatches

7; Conservative

Matches

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Gaps
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OTHER INFORMATION: synthetic peptide (modified form of homo sapiens)
OTHER INFORMATION: sequence)
US-09-798-869-7
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Pred. No. 0.69;
2; Mismatches 3; Indels
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Pred. No. 0.35;
0; Mismatches
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFRENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 1090-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
TYPE: TABLES FASTSED
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                                                        Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/097986 Publication No. US20030022821A1 GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTRIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 54.5%;
Matches 6; Conservative
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Best Local Similarity 63.b.
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US-09-798-869-22
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APPLICANT: (YSTEIN PERCAL
APPLICANT: (YSTEIN PERCAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BLOACITUS PEPTIDES
TITLE FERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASISEQ FOR WINDOWS Version 4.0
SSOFTWARE: PASISEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREUSEQ for Windows Version 4.0
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: HALDIR SYGUND (NSSON)
APPLICANT: HALDIR SYGUND (NSSON)
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                           Sequence 23, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
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Best Local Similarity 63.5-
7; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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                                                            3 CYQWORRMRKL 13
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1 CFAWORAMRKV 11
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; ORGANISM: CAPRINE
US-09-798-869-23
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Score 39; DB
Pred, No. 0.69
2; Mismatches
                                                                                          APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVELNBJ (RNSSON
APPLICANT: LARG VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A4404-PCT-USA-A
FILE REPRENCE: A4404-PCT-USA-A
FILE REPRENCE: A2404-PCT-USA-A
FILE REPRENCE: A2404-PCT-USA-A
FRICK APPLICATION NUMBER: US/99/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1996-08-38
NUMBER FEASTER FOR SEQ ID NOS: 30
SEQ ID NOS: 30
SEQ ID NOS: 30
Application US/09798869
No. US20030022821A1
                         Publication .... GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFAWORAMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: BOVINE
US-09-798-869-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine)
OTHER INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 9; Length 15;
Pred. No. 0.69;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 3
Pred. No. 0.69;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: (YSTEIN REXDAL APPLICANT: (YSTEIN REXDAL APPLICANT: (YSTEIN REXDAL APPLICANT: (YSTEIN REXDAL APPLICANT: LARS VORLAND APPLICANT: LARS VORLAND TITLE OF INVENTION: BIOACTIVE PEPTIDES FILE REFERENCE: A34049-PCT-USA-A CURRENT APPLICATION NUMBER: US/09/798.869 CURRENT APPLICATION NUMBER: PCT/GB99/02851 PRIOR APPLICATION NUMBER: PCT/GB99/02851 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-28 NUMBER OF SEQ ID NOS: 30 SOFTWARE: PSESEE FOR WINDOWS VETSION 4.0 SEQ ID NO 29 LENGTH: 15
                                                                                                              APPLICANT: (YSTEIN REKDAL APPLICANT: OFFNSTALLOWS SUPERING APPLICANT: (YSTEIN REKDAL (RNSSON APPLICANT: EALDUR SVEENBJ(RNSSON APPLICANT: LARS VORLAND: TITLE OF INVENTION: BIOACTIVE PEPTIDES FILE REFERENCE: A34049-PCT-USA-A CURRENT APPLICATION NUMBER: US/09/798,869 CURRENT FILING DATE: 2001-02-21 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-28 NUMBER: OF SEQ ID NOS: 30

SEQ ID NO 8

DENOTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8

LENGTH: 15
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Publication No. US20030022821A1
GENERAL INFORMATION:
                                                    Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
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Best Local Similarity
Matches 6; Conserv
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Length 15;

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RESULT 13
Up-10-013-379-14
Up-10-013-379-14
Sequence 14, Application US/10013379
Publication No. US20020188108A1
Sequence 14, Application US/10013379
Sequence 14, Application No. US20020188108A1
Sequence 14, Application No. US20020188108A1
Sequence 14, Application No. US20020188108A1
Sequence 14, Application No. US20020188108A108A1
Sequence 14, Application No. US20020188108A108A1
Sequence 14, Application No. US20020188108A1
SEQUENCE INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: COMPLEXES OF THE BACTERIAL RIBOSOME CONTAINING TRANSFER RNA
TITLE OF INVENTION: AND MODEL WESENGER RNAS
TITLE OF INVENTION: AND WOODEL US 60/254,603
PRIOR PELICATION NUMBER: US 60/254,603
PRIOR PELICATION NUMBER: US 60/278,013
PRIOR PELICATION NUMBER: US 60/278,013
PRIOR PELICATION NUMBER: US 60/278,013
PRIOR PELICATION NUMBER: 200 60/230
SEQUENCE TILING DATE: 20001-03-22
NUMBER OF SEQ ID NOS: 54
SOCTIVARE: PRET
TYPE: PRT
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2 FAWQRAMRKV 11

CFRWOWRMKKL 13

RESULT 12 US-09-798-869-30

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Sequence 12, Application Us/0895542

SEQUENCE NO. US200017447A1

GENERAL INFORMATION:
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APPLICANT: Shutter, John
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0; Gaps

Score 37; DB 10; Length 2310; Pred. No. 2.6e+02; 0; Mismatches 2; Indels C

Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative

Search completed: February 21, 2003, 08:11:58
Job time : 7.88372 secs

779 CFAWQDRM 786

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1 CFAWQRAM 8

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5.1.3	Compugen
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GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec

US-09-743-107B-95 68 1 CFAWQRAMRKVR 12 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

2: pir2:* 3: pir3:* 4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	lactotransferrin	lactoferrin - g	lactoferrin - sl	ADP, ATP carrier pr	hypothetical prote	Lactoferrin precur	carcinoembryonic	sell cycle arres	hypothetical prote	ohytochrome C -	33.3K hypothetical	methyl-accepting	WTP pyrophosphol	hypothetical prote	pyridoxamine 5'-ph	pyridoxamine 5'	probable pyridoxam		in-2	probable dTDP-4.	gene 20 protein -	ypothetical pro	Deinococcus radiod			ADP, ATP carrier pr	hypothetical pro		Εį
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SUMMARIES	ID	TEHUL	JC2323	852107	G71633	AH3147	A28438	D33876	A39654	AB0858	T14803	G86403	E82395	AC3242	C71306	H97451	AB2670	AG3441	JC1113	S07442	T00104	WZBEM6	C33374	B97374	AH2591	F83199	B97842	T01179	m	JE0238
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οķο	Query Match	83.8	69.1	64.7	63.2	61.8	61.8	58.8	58.8	57.4	57.4	55.9	55.9	54.4		54.4	54.4		54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4		54.4	54.4	54.4
٠.	Score	57	47	44	43		42	40	40	39	39	38	38	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
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hemolysin-type cal	protein F21H11.2 [dynein beta heavy	probable membrane	threonine synthase	hypothetical prote	hypothetical prote	probable secreted	late 100K protein	valine-tRNA ligase	receptor tyrosine	C. elegans protein	hypothetical prote	conserved hypothet	probable phycocyan	hypothetical prote
B82736	D88450	T08030	AD0651	E90238	C86624	H72000	C81357	WMAD15	B71250	T31329	D59433	D83181	AB0438	\$25308	T22597
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16	27	24.	N	m	4	4	ń	807	95	1081	116	174	22	24	275
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37 54.4 16				52.9	52.9		52.9			52.9	52.9	52.9		51.5	35 51.5 27

ALIGNMENTS

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RESULT	Ę	1
SES	FEE	

.actotransferrin precursor [validated] - human

C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S7

Alrede to the EMBL Data Library, March 1994
Alredeance number: G06820
Alredeance number: G06820
Alredeance number: G06820
Alredeance State
A; Molecule type: mRNA
A; Residuces: 1-148, T', 150-422, 'C', 424-711 <REY>
A; Residuces: 1-148, T', 150-422, 'C', 424-711 <REY>
A; Cross-references: EMBL: X53961; NID: g34415; PIDN: CAA37914.1; PID: g34416
A; Cross-references: EMBL: X53961; NI, Malmer, D.; Panella, T.
Mol. Emdocrinol. 6, 1959-1981, 1992
Mol. Emdocrinol. 6, 1959-1981, 1992
A; Title: Differential molecular mechanism of the estrogen action that regulates lactofe
A; Reference number: A45401; MUID: 93125571; PMID: 1480183

Accession: A45401

A;Nolecule type: DNA
A;Residues: 1-15 <TEN>
A;Cross-references: GBS-S2659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Cross-references: GBS-S2659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:122202)
B;Powell, M.J.; Ogden, J.E.
Nucleic: Acids Res 18, 4013, 1990
A;Title: Nucleotide sequence of human lactoferrin cDNA.
A;Reference number: S10324; MUID:90326549; PMID:2374734

Molecule type: mRNA Residues: 3-711 <POW>

Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412; Stcowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.; A9-355, 1991 cochem. J. 276, 349-355, 1991 fitle: Expression of cloned human lactoferrin in baby-hamster kidney cells. Reference number: S15853; MUID:91264786; PMID:2049066

Status: nucleic acid sequence not shown; not compared with conceptual translation

A, Molecule type: protein A, Residues: 20-28, 'X', 30-31 <ST2>

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AH3147
hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens
C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AH3147
C;Accession: AH3147
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCle.
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A;Cross-references: GB:AJ235273; GB:AJ235269; NID:g3861237; PIDN:CAA15167.1; PID:g3861;
A;Experimental source: strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                   lactoferrin - sheep (fragment)

C, Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C, Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C, Species: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997

C, Accession: S52107

B, Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

B; Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

B; Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

B; Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.

A; Reference number: S52107; MUID:95127729; FMID:7827104

A; Reference number: S52107; MUID:95127729; FMID:7827104

A; Residues: 1-35107

A; Residues: 1-33 < QIA>

C; Superfamily: transferrin; transferrin repeat homology

C; Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C,Accession: G71633
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: G71633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP,ATP carrier protein (11c5) RP739 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
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                              Length 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 33;
                                                                                                       2; Indels
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                                      2
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Pred. No. 0.28;
3; Mismatches
                              Score 47; DB:
Pred. No. 1.5;
2; Mismatches
                              69.1%;
ilarity 63.6%;
Conservative 2
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Best Local Similarity 54.5%;
Matches 6; Conservative
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482 CFAWIYAVRKI 492
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                                                                                                                                                                                                                       38 CYQWQRRMRKL 48
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                                  Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Residues: 436-487, 'A', 489-711 <RAD>
A; Cross-references: EMBLAMS 4862; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyths. A; Reference number: A61169; MUID:91235214; PMID:1674448
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(Experimental source: normal breast tissue)
(Experimental source: normal breast tissue)
(Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
ur. J. Biochem. 145, 659-666, 1984
(Mille: Human lactotransferrin: amino acid sequence and structural comparisons with oth Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein ;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4;Note: this is the final paper in a series ;Note: this is the final paper in a series ;Note: this is the final paper in a series ;Note: G'; Hoegdall, E.V.; Barkholt, V.; Norskov, L. ur. alochem. 241, 303-308, 1996 ;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin ;Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Map position: 3q21-3q23
C,Superfamily: transferrin, transferrin repeat homology
C,Keywords: duplication; glycoprotein; iron binding; milk
C,Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-71/Product: lactoriansferrin status experimental <MAT>
F;20-71/Product: lactoriansferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-699/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;57,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Title: Isolation of lactoferrin cDNA;Reference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
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A,Residues: 1-708 <LEP>
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication; glycoprotein
F,359-696/Domain: transferrin repeat homology <TRH2>
F,252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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R, Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Blochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A; Title: Characterization of the goat lactoferrin DNA: A; Reference number: JC2323; MUID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: not compared with conceptual translation
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Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
Experimental source: neutrophil granulocytes
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Best Local Similarity
Matches 10; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
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hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
A,Note: this species has also been called Salmonella typhi
C,Date: 09.Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C,Accession: AB0858
R,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche R,Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churche K,P. T.; Connerton, P.; Connin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra Nature 413, 488-852, 2001
Nature 413, 488-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servales and the complete servale
   A;Reference number: A33876; MUID:89214106; PMID:2708349
A;Accession: D38876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <ROD>
A;Cross-references: GB:M60026; NID:g203407; PIDN:AAA40911.1; PID:g554427; GB:J04626; C
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-term
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell cycle arrest protein BUB2 - yeast (Saccharomyces cerevisiae)

N;Alternate names: protein YM796.08c; protein YMR055c

C;Species: Saccharomyces cerevisiae

C;Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text_change 21-Jul-2000

C;Accession: A39654; S54555; $19034

R;Hoyt, M.A.; Totis, L.; Roberts, B.T.

Cell 66, 507-517, 1991

A;Rtle: Saccharomyces cerevisiae genes required for cell cycle arrest in re
A;Reference number: A39654; MUID:91330299; PMID:1651171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; cross-references: GB:M64706; NID:gl71133; PIDN:AAA16885.1; PID:gl71135 R;Devlin, K.; Churcher, C.M. submitted to the EMBL Data Library, May 1995
                                                                                                                                                                                                                                                                                                        Length 114;
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12;
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Pred. No. 4.8;
2; Mismatches
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A.Cross-references: SGD:S0004659, MIPS:YMR055c
A.Map position: 13R
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                                                                                                                                                                                                                                                                                                    58.8%;
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Best Local Similarity 60.0
Matches 6; Conservative
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Les 6; Conservative
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A;Accession: S54555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-306 < HOY>
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A; Residues: 1-306 <DEV>
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42 FAWYRGLRKI 51
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Best Local S
Matches 6
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R;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A/Titler Lactotransferrin is the major estrogen inducible protein of mouse uterine secre A;Reference number: A92596; MUID:87280033; PMID:3611056
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D33876
carcinoembryonic antigen homolog 4 - rat (fragment)
ciscoembryonic antigen homolog 4 - rat (fragment)
c;Species: Rattus norvegicus (Norway rat)
c;Species: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C;Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 23-Jul-1999
C;Accession: D33876
R;Kodelja, V; Lucas, K; Barnert, S; von Kleist, S; Thompson, J.A.; Zimmermann, W.
J. Biol. Chem. 264, 6906-6912, 1989
A;Title: Identification of a carcinoembryonic antigen gene family in the rat. Analysis
                                                                                                                  ster, E.W.
Ajītle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
AjReference number: AB2577; PMID:11743193
AjAccession: AH3147
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                                                                                                                                                                                                                                                                                                                                                                           Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187; Experimental source: strain C58 (Dupont)
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Biol. Chem. 266, 21880-21885, 1991
Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
Reference number: A41205, MUID:92042099; PMID:1939212
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S.Species: Mus musculus (house mouse)
S.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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7:2-0-70/Product: lactotransferrin #status predicted <MAT>
F:358-655/Domain: transferrin repeat homology <TRH2>
F:358-651/Domain: cransferrin repeat homology <TRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 12;
0; Mismatches 4; Indels
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Superfamily: transferrin, transferrin repeat homology
Keywords: duplication; glycoprotein
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Pred. No. 2
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63.6%;
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Residues: 3-707 <PEN>
Cross-references: EMBL:J03298
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es 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-121 <KUR>
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Residues: 1-15 <LIU>
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Gaps

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methyl-accepting chemotaxis protein VCA0974 [imported] - Vibrio cholerae (strain N169. C;Species: Vibrio cholerae
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82395
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.Chardson, D.; Ermolawa, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Teleron on maber: A82035; MUID:20406833; PMID:10952301
A;Accession: E82295
A;Accession: E82295
A;Accession: DNA
A;Residues: 1-561 <HEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE004423; GB:AE003853; NID:99658400; PIDN:AAF96870.1; GSPDB:GN:A;Experimental source: serogroup O1; strain N16961; biotype El Tor
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-161
A,CKUR>
A,Cesidues: 1-161
A,CTOSS-references: GB:AE008690, PIDN:AAL46353.1, PID:g17744142, GSPDB:GN00189
A,Experimental source: strain C58 (Dupont)
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hypothetical protein TP0594 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%; Score 38; DB 2; Length 561; 63.6%; Pred. No. 51; ive 1; Mismatches 3; Indels
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                                                                CFTWEEYARHVR 19
                 CFAWQRAMRKVR 12
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Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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51 AWEAALREVR 60
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A;Genome: plasmid
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Cipectes: Arabidopsis thaliana (Mouse-ear cress)
Cipectes: Arabidopsis thaliana (Mouse-ear cress)
Cipectes: O. Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
Cipacession: G86403
R.Theologis, A.; Ecker, J. R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.Theologis, A.; Ecker, J. R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R.F.; Hudres, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Akuthors: Hunter, V.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Martin, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Liu, S.A.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rajathore: Salzbergy, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Rajathore: Salzbergy, S.L.; Schwartz, J.C.; Davis, R.W.
A; Multile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MulD:21016719; PMID:11130712
A; Scatus: preliminary
A; Molecule type: DA.
A; Aldolecule type: DA.
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phytochrome C - sorghum
C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor (sorghum)
C;Accession: T14803
R;Childs, K.L.; Miller, F.R.; Cordonnier-Pratt, M.M.; Fratt, L.H.; Morgan, P.W.; Mullet, submitted to the EMBL Data Library, April 1996
A;Reference number: Z18186
A;Accession: T14803
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1135 <-CHI>
A;Residues: 1-1135 <-CHI>
A;Cross-references: EMBL:U56731; NID:g1800218; PID:g1800219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: phytochrome, phytochrome homology
C;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regulat
F;65-581/Domain: phytochrome homology <PHY>
F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
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A;Residues: 1-511 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176 C;Genetics: A;Gene: STY3070
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A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
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Pred. No. 66;
                                                                                                                                                                           Score 39; DB 2; Length 511;
Pred. No. 31;
0; Mismatches 5; Indels
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Pred. No. 27;
1; Mismatches 5; Indels
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Best Local Similarity 50.0%;
Matches 6; Conservative
                                                                                                                                                                              Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
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Best Local Similarity 45.5%
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24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999

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'Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin son, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc hey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
cience 281, 375-388, 1998
'Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. Racession: C71306
'Reference number: A71250; MUID:98332770; PMID:965876
'Status: preliminary; nucleic acid sequence not shown; translation not shown 'Molecule type: DNA
'Residues: 1-202 <CCL>
'Residues: 1-202 <CCL>
'Residues: GB:AE001234; GB:AE000520; NID:93322881; PIDN:AAC65572.1; PID:9332289; Experimental source: strain Nichols
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C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
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Nolecule type: DNA
KBeidues: 1-206 <KUR>
Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.4%; Score 37; DB 2; Length 202; 87.5%; Pred. No. 29;
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A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
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Best Local Similarity 87.5
Matches 7; Conservative
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homo sapien methylobaci pyrobaculum pinus sylve drosophila mycobacteri

mus musculu influenza b

Q111059 P21159 Q9Cx47 P015743 Q157443 Q827143 Q41046 Q24595 Q50651

mycobacteri myxococcus

cvanidium

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Cho Y.Y.;
Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactofransferrin precursor (Lactoferrin) (Contains: Lactoferroxin A, LIF OR LF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Mammary gland;
MEDLINE=90384839; PubMed=2402455;
MEDLINE=90384839; PubMed Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Mammary gland;
Liang Q., Jimenz=Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Bone marrow;
Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region DNA
                                                                                                                                                                                                                                                                                                      TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Mammary gland;
Cheng H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
[8]
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conneely O.M.; Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                         ALIGNMENTS
                                         PDXH MYXXA
XRC2 MOUSE
VNS1 INBLE
GP68 HUMAN
DHOM METGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Mammary gland;
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ID TRRE H

AC 096K258

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DT 15-JUUL

DT 15-JUUL

DT 15-JUUL

DE Lactot

CON LIFTON

CON MAMMAIN

CON NUBL T

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RA REY M.

RA REY M.

RA COMPE

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human adeno
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Q9tum0 camelus dro
Q29477 capra hircu
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PHYC_SORBI
ILLA BOYN
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WD66_PHYPO
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria R., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.,
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MEDLINE=90064528; PubMed=2585506;
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Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
Jolles P.;
                                                                                                                                                                                                                                                                                                                                             Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J., Jolles P.;
Jan 88 amino acid long C-terminal sequence of human
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MEDLINE-88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
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                                                                                     SEQUENCE OF 20-711.

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comparisons with other transferzins.";
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Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
        TISSUB-Mammary gland;
MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
Nucleic Acids Res. 18:4013-4013(1990);
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MEDLINE=97156796; PubMed=9003186;
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MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 609-711.
MEDLINE-82262043; PubMed=7049727;
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SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ifo K., Chiba H., Yoshikawa M.;
"Isolation and characterization of oploid antagonist peptides derived from human lactoferrin.";
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
'Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-99192677; PubMed=10089508;
Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
"Structure of human apolactoferrin at 2.0-A resolution. Refinement and analyais of ligand-induced conformational change.";
Acta Crystallogr. D 54:1319-1335(1998).
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SUBCELLUTAR LOCATION: Secreted.
DOMAIN: COMPOSED OF TWO HONOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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EMBL; U07643; AAB60324.1; --
EMBL; M93150; AAA36159.1; --
EMBL; M93202; AAA55511.1; --
EMBL; M93205; AAA56656.1; --
EMBL; M18642; AAA86665.1; --
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X52941; CAA37116.1;
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Camelus dromedarius (Dromedary) (Arabian camel).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                       STRAIN-Somali; TISSUB-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; Irk001156; Transferrin.
Pfam; PF00405; transferrin; 2.
SMART; PR00421; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00205; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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        83.8%; Score 57; DB 1; Length 711;
83.3%; Pred. No. 0.0052;
iive 0; Mismatches 2; Indels
                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN
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                                                                                           RESULT 2
TRFL CAMDR
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500 AA

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SEQUENCE FROM N.A.
STRAIN-Madrid E;
MEDLINE-99039499 bubMed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                        Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                   15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
ADP,ATP carrier protein 5 (ADP/ATP translocase 5)
                                                                                                                                                                                                                                                                     SEQUENCE OF 325-500 FROM N.A.
                                                                                                                                                                                                                                                 Nature 396:133-140(1998).
                                                                                                                 Rickettsia prowazekii
                                          RICPR
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way endified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                        InterPro; InterPro; Iransferrin.
Pfam; PF00405; transferrin.
PFAMI; PF00405; transferrin.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN.
PROSITE; PS00205; TRANSFERRIN.
PROSITE; PS00207; TRANSFERRIN.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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(POTENTIAL).
(POTENTIAL).
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L -> R (IN REF. 2).
F -> P (IN REF. 2).
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N-LINKED (GLONAC...)
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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63.6%;
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EMBL; X78902; CAA55517.1; -.
HSSP; O77698; 1CE2.
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708 AA;
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Pred. No. 1.4;
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InterPro; IPRO04667; ADP_ATP_car.
Pfam; PF03219; TLC; 1.
IIGREPMS; TG070769; AAA; 1.
Transmembrane; Transport; ATP-binding; Multigene family;
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Hoyt M.A., Totis L., Roberts B.T.,
"S. cerevisiae genes required for cell cycle arrest in response to
loss of microtubule function.";
Cell 66:507-517(1991).
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SEQUENCE FROM N.A.
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"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885 (1991)
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OP AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE 87280033; PubMed=3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse.
                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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SUBCELLULAR LOCATION: SECTETED.
SUBCELLULAR LOCATION: SECTETED.
SUBCELLULAR LOCATION: SECTETED.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                 TREL MOUSE STANDARD; PRT; 707 AA. P8071; P7059; Q61799; Q92222; 01-AUG-1988 (Rel. 08, Created) PUN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
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EMBL; D88510; BAA13633.1; --
EMBL; BC068904; AAA66894.1; --
EMBL; M74778; AAA39427.1; --
PIR; A28438; A28438.
HSSP; P02788; 1CB6.
MGD; MGI:96837; LCB6.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin.
PRINIS; PR00422; TRANSFERRIN.
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PROSITE; PS00205; TRANSFERRIN 1; 1.

PROSITE; PS00206; TRANSFERRIN 2; 2.

PROSITE; PS00207; TRANSFERRIN 3; 2.
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                            482 CFAWIYAVRKI 492
  1 CFAWQRAMRKV 11
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1902 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaces;
NCBI_TaxID=4932;
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Pred. No. 3.1;
0; Mismatches 4; Indels
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63.6%;
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Matches 7, Conservative
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SEQUENCE FROM N.A.
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Plant Physiol. 113:611-619(1997).
Plant Physiol. 113:611-619(1997).
Plant Physiol. 113:611-619(1997).
ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTROM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PPR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                               "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                     regulates cytokinesis.";
J. Cell Sci. 114:2345-2354(2001).
-!- FUNCTION: Part of a checkpoint which monitors spindle integrity and prevents premature exit from mitosis. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFA1/BUB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.B.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                           MEDLINE-21385309; PubMed=11493673;
Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D.,
Johnston L.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.8%; Score 40; DB 1; Length 306; 60.0%; Pred. No. 3.1; ive 1; Mismatches 3; Indels
STRAIN=S288c / AB972; Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 AA; 35027 MW; AIDDBFB548E81EA3 CRC64;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Phytochrome C.
                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: Interacts with BFA1.
-!- SUBCELLULAR LOCATION: Spindle poles.
-!- SIMILARITY: TO S.POMBE CDC16.
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EMBL, 249703; CAA89765.1; -.
PIR, 339654; A39654.
SGD; S0004659; BUB2.
INCERPYO; DRA000195; RabGAP_TBC.
Pfam; PP00566; TBC; 1.
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Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell cycle, Mitosis.
SEQUENCE 306 AA:
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MEDILNE=92241682; PubMed=1572550;

MEDILNE=92241682; PubMed=1572550;

MEDILNE=92241682; PubMed=1572550;

MEDILNE=92241682; PubMed=1572550;

MEDILNE=92241682; PubMed=1572550;

MILARITY: Williamson M.L., McConnell I.;

Gene 113:283-284(1992).

Gene
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                                                                                                                        Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
          01-AUG-1992 (Rel. 23, Last sequence update)
01-RB1-1996 (Rel. 33, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PSS) (TAC antigen) (CD2S).
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NS SIMILARITY.
INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
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SUSHI 1.
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N-LINKED (GLCNAC.
S -> T (IN REF. 2)
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EMBL; X60149; CAA42723.1; -.
EMBL; A19167; CAA01447.1; -.
PIR; S18899; S18890.
PIR; J1113; JC1113.
HSSP; P01589; IILM.
INTERPO; IRRO00436; Sushi_SCR_CCP.
PEam; PP00084; sushi; 2.
EMBRT; SM00032; CCP; 2.
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                                                                                                                                                                                                                                                                                                       rissum=T-cell;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                              MEDLINE=96116968; PubMed=8563178;
MEDLINE=96116968; PubMed=8563178;
MEDLINE=96116968; PubMed=8563178;
Too J., de Leon F.A., Stone R.T., Beattie C.W.;
"Cloning and chromosomal assignment of the bovine interleukin-2 receptor alpha (IL-2R alpha) gene.";
Mamm. Genome 6.751-753(1995).
-! FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-! SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE MITTHEN GAMMA CHAIN.
                                                                                                                                          MEDLINE-88212503; PubMed=2835311;
MEDLINE-88212503; PubMed=2835311;
Melinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.;
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
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Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Ammania; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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EXTRACELLULAR (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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Pred. No. 10;
1; Mismatches 5; Indels
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EMBL; U24226; AAC46487.1; -.
FIR; S07442; S07442.
HSSP; P01589; IILM.
INTERPRO; IPRO00436; Sushi_SCR_CCP.
Fam; PRO0064; sushi; 2.
SMART; SM00032; CCP; 2.
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Best Local Similarity 50.0%;
Matches 6; Conservative
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122
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275 AA;
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AC P26898;
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SEQUENCE
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Gaps

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01-AUG-1992 (Rel. 23, Created)

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Length 275; 5; Indels

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Q9ZWT9; P93429;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                     EMBL, U86011, AAC26321.1; -.
InterPro; IPR001680, WD40.
PEAM; PR00400; WD40; 10.
PRINTS; PR00320; GPROTEINBRPT.
SWART; SW00320; WP46; 10.
PROSITE; PS00678; WD REPEATS 1; FALSE_NEG.
PROSITE; PS50284; WD_REPEATS_2; 6.
PROSITE; PS50284; WD_REPEATS_2; 6.
PROSITE; PS50284; WD_REPEATS_2; 6.
REPEAL; WD_REPEATS_2; 6.
REPEAL
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Best Local Similarity
Local 5; Conserva
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601 AA;
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"A novel 66-kDa stress protein, p66, associated with the process of yest formation of Physarum polycephalum is a Physarum homologue of a yeast actin-interacting protein, AIPI.";
J. Blochem. 124:326-331(1998).
-!- FUNCTION. ASSOCIATED WITH PEPROCESS OF CYST FORMATION.
-!- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS).
-!- SIMILARITY: BELONGS TO THE AIPI FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                              15-JUL-1999 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
66 Mba stress protein (p66).
Physarum polycephalum (Slime mold).
Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;
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Pfam; PF01646; Herpes UL24; 1.
SEQUENCE 303 AA; 34942 MH; DF6D59F7A1C83A0B CRC64;
                                                                                                                                  Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
                                       303 AA
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                                       PRT;
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MEDLINE=98351989; PubMed=9685722;
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                                       STANDARD;
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P90587;
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UL24_HSVSA
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WD66_PHYPO
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Mol. Biol. BYOL. 13:1141-1150(1996).
Mol. Biol. BYOL. 13:1141-1150(1996).

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FRA REGION. PHOTOCONVERSION OF PR INDECES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR IN PRECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE
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Tahhr M., Kanegae H., Takano M.;
"Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence.";
(In) Plant Gene Register PGR98-210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Rukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Enrhartoideae, Oryzeae, Oryza
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MRDLINES-97019052, PubMed=8865668;
Mathews S., Sharrock R.A.;
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot analossers.";
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MD 2.
MD 3.
MD 4.
MD 5.
MD 7.
MD 9.
MD 10.
MD 10.
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Embryophyta; Tracheophyta; edons; core eudicots; Rosidae;

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STRAIN=CV. Columbia,
MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. X. St
features of the regions of 3,076,755 bp covered by sixty Pl and
                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core e
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
        Arabidopsis thaliana (Mouse-ear cress)
                                                                  SEQUENCE FROM N.A.
                                              NCBI_TaxID=3702;
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ranscription regulation; Photoreceptor; Phytochrome; Chromophore;
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F -> S (IN REF. 2).
C -> S (IN REF. 2).
WW; F2A520181CFE7B32 CRC64;
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PAS 2.
HISTIDINE KINASE.
                                                                                                                                                                                                                     EMBL, UGLZU/; ARMSHINDE.1, ...
INTERPRO; IPR003594; ATPDING ATPRSE.
INTERPRO; IPR003018; GAF.
INTERPRO; IPR003601; HIS KIN Sig.
INTERPRO; IPR003601; HIS KIN Sig.
INTERPRO; IPR000014; PAS.
INTERPRO; IPR000014; PAS.
INTERPRO; IPR0001294; Phytochrome.
Pfam, PF00360; phytochrome; I.
Pfam; PF00380; phytochrome; I.
Pfam; PF00381; signal; 1.
Pfam; PF00389; ASF, 1.
Pfam; PF00389; ASF, 1.
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PROSITE; PS50112; PAS; 2.
PROSITE; PS001245; DEUMANTE
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PROSITE; PS50046; PHYTOCHROME 2; 1.
                                                                                                                                                                                                       EMBL; AB018442; BAA74448.1; -.
EMBL; U61207; AAR41996 1. -
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SMART; SM00387; HATPase c; 1.
SMART; SM00388; HisKA; I.
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Conservative
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SMART; SM00091; PAS; 2.
TIGRFAMB; TIGR00229; SE
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1137 AA;
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les 5; Conserv
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PROSITE; PS00154; ATPASE E1 E2; 1.
Hydrolase; Transmembrane; Phosphorylation; ATP-binding; Metal-binding;
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44.4%; Pred. No. 45;
ive 4; Mismatches 1; Indels
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EXTRACELLULAR (POTENTIAL)
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InterPro; IPR001757; ATPase E1-E2.
InterPro; IPR01454; HIgnase/hydrlase.
Pfan; PF00122; E1-E2 ATPase; 1.
Pfan; PF00702; Hydrolase; 1.
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1179 AA; 131115
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Best Local Similarity
Matches 4; Conserv
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Gaps

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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Potential cation-transporting ATPase (EC 3.6.3.-).
ATSG23630 OR MQM1.11.

PRT; 1179 AA

STANDARD;

ATX1_ARATH ID ATX1_ARATH AC Q9LT02;

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"Retinal stimulates ATP hydrolysis by purified and reconstituted ABCR, the photoreceptor-especific ATP-binding cassette transporter responsible for Stargardt disease.";
J. Biol. Chem. 274:8269-8281(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cremers F.P.M., van de Pol D.J.R., van Driel M.A., den Hollander A.I., van Haren F.J.J., Knoers N.V.A.M., Tijmes N., Bergen A.A.B., Rohrschneider K., Blankenagel A., Pinckers A.J.L.G., Deutman A.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97207641; PubMed=9054934;
Allimets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
Allimets R., Singh N., Sun H., Shroyer N.F., Hutchinson A.,
Chidambaram A., Gerrard B., Baird L., Stauffer D., Peiffer A.,
Rattner A., Smallwood P.M., Li Y., Anderson K.L., Lewis R.A.,
Nathans J., Leppert M., Dean M., Lupski J.R.,
"A photoreceptor cell-specific ATP-binding transporter gene (ABCR) is
mutated in recessive Stargardt macular dystrophy.";
Nat. Genet. 15:236-246(1997).
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MEDLINE=99163759; PubMed=9503029;
Gerber S., Rozet J.-M., van den F. J. R., Hoyng C.B., Munnich A.,
Blankenagel A., Kaplan J., Cremers F.P.M.;
"Complete exon-intron structure of the retina-specific ATP binding transporter gene (ARCR) allows the identification of novel mutations underlying Stargardt disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE=97345663; PubMed=9202155; Azarian S.M., Travis G.H.; Azarian S.M., Travis G.H.; The photoroceptor rim protein is an ABC transporter encoded by the gene for recessive Stargardt's disease (ABCR)."; FEBS Lett. 409:247-252(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS STGD.
MEDLINE-98141123; PubMed=9490294;
Nagonkin I., Illing M., Koehler M.R., Schmid M., Molday R.S.,
Weber B.H.F.;
                                                                                                                                                                              ABCR HUMAN STANDARD, PRT, 2273 AA.
P78363; O60438; O60915; O15112;
30-MAY-2000 (Rel. 39, Created)
15-UN-2002 (Rel. 39, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Last annotation update)
15-UN-2002 (Rel. 41, Rest annotation update)
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[7]
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                                1144 CYSWERLLR 1152
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1 CFAWORAMR 9
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VARIANTS STGD E-60; T-60; E-65; L-68; R-72; C-212; S-230; S-247; V-328; K-471; P-541; Q-572; R-607; K-635; C-653; Y-764; R-765; A-901; L-959; K-1036; V-1038; P-1063; D-1087; C-1097; C-1108; L-1380; K-1399; P-1430; V-1440; H-1443; L-1486; Y-1488; M-1537; P-1689; L-1705; T-1733; R-1748; P-1763; K-1885; H-1898; E-1961; R-1975; S-1977; G-2077 W-2077 AND V-2241, AND VARIANTS Q-152; H-212; R-423; I-552; R-914; Q-943; T-1562; I-1868; M-1921; L-1948; F-1970; A-2059; N-2177 AND
                                                                                                                                                                                                                                                                         "A comprehensive survey of sequence variation in the ABCA4 (ABCR) gene in Stargardt disease and age-related macular degeneration."; Am. J. Hum. Genet. 67:800-813 (2000).
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MEDLINE-20114952; PubMed-110711710;
Simonelli F., Testa F., de Crecchio G., Rinaldi E., Hutchinson A., Atkinson A., Dean M., D'Urso M., Allikmets R.;
"New ABCR mutations and clinical phenotype in Italian patients with Stargardt disease.";
Invest. Ophthalmol. Vis. Sci. 41:892-897(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS STGD ASP-340; GLN-572; ALA-863; SER-965; VAL-1038; ALA-1780 AND HIS-1898, AND VARIANT GLN-943.

MEDLINE-20208356; PubMed=10746557;
Shroyer N.F., Lewis R.A., Lupski J.R.;
Shroyer N.F., Lewis R.A., Lupski J.R.;
Gomplex inheritance of ABCR mucations in Stargardt disease: linkage disequilibrium, complex alleles, and pseudodominance.";
Hum. Genet. 106:244-2448(2000).
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Papaioannou M., Ocaka L., Bessant D., Lois N., Bird A.C., Payne A.,
Baptacharya S.S.;
"An analysis of ASCR mutations in British patients with recessive retinal dystrophies.";
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MEDLINE=20472331; PubMed=11017087;
Sun H., Smallwood P.M., Nathans J.;
"Biochemical defects in ABCR protein variants associated with human
                                                                                                                                                                               MEDLINE=20442027; PubMed=10958763;
Rivera A., White K., Stoehr H., Steiner K., Hemmrich N., Grimm T.,
Jurklies B., Lorenz B., Scholl H.P.N., Apfelstedt-Sylla E.,
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MEDLINE-21478761; PubMed=11594993;
Eksandh L., Ekstroem U., Abrahamson M., Bauer B., Andreasson S.;
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                                                                                                                                                                                                                                                                                                                                                                 VARIANTS CORD3 GLU-65, CYS-212; PRO-541; ALA-863; GLY-863 DEL; VAL-1038; LYS-1122; TYR-1490 AND ASP-1598.
MEDLINE-20442040; PubMed=10958761;
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Pred. No. 89;
0; Mismatches 2; Indels
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nvest. Ophthalmol. Vis. Sci. 41:16-19(2000).
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InterPro; IPR004273; Dynein heavy. Pfam; PF03028; Dynein heavy; 1. Motor protein; Microtubules; Dynein; ATP-binding; Flagella;

EMBL; U02963; AAA19956.1;

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MICROTUBULE-BINDING (POTENTIAL).
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3425 3425 3728 1926 2209 2537 2886

NP_BIND NP_BIND NP_BIND

NP BIND DOMAIN

chain genes.",
J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
-!- FUNCTION: PORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.

DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.

STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy

Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales, Chlamydomonadaceae, Chlamydomonas.

Chlamydomonas reinhardtii.

SEQUENCE FROM N.A. NCBI_TaxID=3055

01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Dynain beta chain, flagellar outer arm. ODA4 OR ODA-4 OR SUP1.

STANDARD;

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                               Score 37; DB 1; Length 4568; Pred. No. 1.8e+02; 4; Indels 3; Mismatches 4; Indels
   MW; 9A9A5393C7C36AE7 CRC64;
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38 AA.
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Q8TCD2
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Q9tuy5 homo sapien
Q9tu80 ovis aries
Q8ti6k3 agrobacteri
G51104 rattus norv
G53112 rattus norv
Q53462 salmonella
Q59ws6 lycopersico
Q97662 arabidopsis
Q98gw4 thizobium l
Q9kvt6 homo sapien
Q9bvt6 homo sapien
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Maximum DB seq length: 200000000
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                                                                                                                                          February 21,
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Q80618 agrobacteri
Q80610 rhizobium 1
Q80610 rhizobium 1
Q92rh8 rhizobium m
Q97kB rhizobium m
Q97kB rhizobium m
Q91kB artinobacil
Q91g9 actinobacil
Q91g9 actinobacil
G6251 actinobacil
G6251 actinobacil
G6015 agrobacteri
G8015 sarobacteri
Q8015 sarobacteri
Q8015 ricketsia
G8037 oryziae lat
Q9031 ricketsia
G6237 arabidopsis
G6527 arabidopsis
G9745 caenorhabdi
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29ups0 homo sapien
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.; Straubberg R.; Straubberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH222347.1; -. SEQUENCE 711 AA; 78327 MW; IB9C7EE097C45FAF CRC64;
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Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raywond C., Rouse G., Saemphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gradon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester B.W.;
Nester B.W.;
Nester B.W.;
CLUMILEY F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester B.W.;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=BD II, TISSUE=LIVER;
MEDLINE=89214106; PubMed=2708349;
Kodelja V., Lucas K., Barnert S., von Kleist S., Thompson J.A.,
Zimmermann W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of a carcinoembryonic antigen gene family in the Analysis of the N-terminal domains reveals immunoglobulin-like, hypervariable regions.", "J. Biol. Chem. 24:596-6912(1989), EMBU, M60026, AAA40911.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.8%; Score 42; DB 16; Length 121; 63.6%; Pred. No. 4.8; tive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE009409; AAL45598.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 121 AA; 14085 MW; EBAF41617A3CEA53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA; 12832 MW; 3AE108689B061686 CRC64;
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UNOV-1996 (TrEMBLrel. 01, Created)
01-7AN-1999 (TrEMBLrel. 09, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
Carcinoembryonic antigen-related protein (Fragment)
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Carcinoembryonic antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                      Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 61.8
Best Local Similarity 63.6
Matches 7; Conservative
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Q63104
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963112
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 17, Last annotation update)
12ctoferrin (Fragment).
12ctoferrin (Fragment).
12ctoferrin (Fragment).
12ctoferrin (Fragment).
13ctoferrin (Fragment).
14ctoferrin (Fragment).
15ctoferrin                                                                                                                                                                                                                                          "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21608550; PubMed=11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobacterium tumefaciens (strain CS9 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
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                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n 70.6%; Score 48; DB 4; Length 38; Similarity 81.8%; Pred. No. 0.13; 9; Conservative 0; Mismatches 2; Indels
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Pred. No. 0.56;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
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MEDLINE=95127729; PubMed=7827104;
MEDLINE=95127729; PubMed=7827104;
Blochim. Blochys. Acta 1243:25-32 (1995).
HSSP; O77698; 1CE2.
InterPro; IPRO1156; Transferrin.
Pfam; PPO0405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Atu4804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA
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                                                                                                                                                                                                                                                                   seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
Sato I.;
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54.5%;
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Matches 6; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                              NCBI_TaxID=9606;
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QBUEK3;
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MEDLINE=99413290; PubMed=10485280;
Kerckhoffs L.H., Kelmenson P.M., Schreuder M.E., Kendrick C.I.,
Kendrick R.E., Hanhart C.J., Koornneef M., Pratt L.H.,
Cordonnier-Pratt M.M.,
"Characterization of the gene encoding the apoprotein of phytochrome
B2 in tomato, and identification of molecular lesions in two mutant
                                                                                                                                                         Lycoperation esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

NCBL_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
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PROSITE; PS00061; ADH SHORT; UNKNOWN_1.
PROSITE; PS00245; PHYTOCHROME_1, 1.
PROSITE; PSS0046; PHYTOCHROME_2; 1.
SEQUENCE 1121 AA; 125308 MW; ED9EDA704BB37F27 CRC64;
                                          (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last sequence update)
Last annotation update)
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54.5%; Pred. No. 1.6e+02;
iive 1; Mismatches 4.
  PRT; 1121 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             alleles.";
Mol. Gen. Genet. 261:901-907(1999).
EMBL; AF122901; AAD50631.1; -.
InterPro; IPR002198; ADH short.
InterPro; IPR003594; ATPbind_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000014; PAG domain.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAP; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00389; PAS; 2.
Pfam; PF00380; pAytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003661; His kinA.
IPR004359; HIS KIN sig.
IPR001610; PAC.
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SMART; SM00387; HATPASS C; 1.
SMART; SM00388; HisKA; I.
SMART; SM00086; PAC; 1.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 54.9
les 6; Conservative
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00388;
SMART; SM00086;
SMART; SM00091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
                                                                                                               Phytochrome B2.
PHYB2.
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                                          01-MAY-2000
01-MAY-2000
01-JUN-2002
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InterPro;
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InterPro;
InterPro;
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9SMS60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    087054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                      SEQUENCE FROM N.A.

STRAIN-SPRAGUS-DAWLEY, TISSUE=LIVER;

STRAIN-SPRAGUS-DAWLEY, TISSUE=LIVER;

MEDLINE-90243655; Pubmed-2335509;

Rebstock S., Lucas K., Thompson J.A., Zimmermann W.;

"CDMA and gene analyses imply a novel structure for a rat

"Carcinoembryonic antigen-related protein.";

"Carcinoembryonic antigen-related protein.";

"Carcinoembryonic antigen-related protein.";

"MA2475; AAA66038.1; -.

"InterPro; IPR003599; IG."

"InterPro; IPR003069; IG.MHC.

"SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.8%; Score 40; DB 11; Length 234; 60.0%; Pred. No. 22; 2; Indels ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57:4%; Score 39; DB 16; Length 511; 58.3%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                        Rebstock S., Lucas K., Thompson J.A., Zimmermann W.A.,
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA; 26171 MW; 69BBC9EE0C773F2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AL677276; CAD06049.1; -. Hypothetical protein; Complete proteome. SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        511 AA
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                                  STRAIN-SPRAGUE-DAWLEY, TISSUE-LIVER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFAWORAMRKVR 12
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 7; Conser
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NCBI_TaxID=601;
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Q8Z462; Q8Z462

RESULT 7 **08**2462

Query Match

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Indels

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Query Match

Best Loca Matches

à 엄 RESULT 8 Q9SWS6

STRAIN=Z17561; Fallarino A.;

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Q9C6N2

RESULT 10

Q9C6N2

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SEQUENCE FROM N.A.
STRAIREL TOR NIGS61 / SERCITYPE 01;
MEDLINE=21 TOR NIGS61 / Dubwed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Raed T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                      Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawabhima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabatu S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.9%; Score 38; DB 16; Length 329; 60.0%; Pred. No. 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 561;
                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein; Complete proteome.
SEQUENCE 329 AA; 34754 MW; 78FC399867P6F3D2 CRC64;
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Last annotation update)
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                 MEDLINE=21082930; PubMed=11214968;
                           Phyllobacteriaceae, Mesorhizobium.
NCBI_TaxID=381,
                                                                                                                                                                                                                                                                                                                       EMBL; AP003001; BAB50102.1; -. InterPro; IPR003760; Bmp. Pf02608; Bmp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
EMBL; AE004423; AAF96870.1; -.
HSSP; P02942; 1QU7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPB1gnal; 1.
PRINTS; PR002060; CHEMTRNSDUCR:
SMART; SM00304; HAMP; 1.
SMART; SM00283; MA; 1.
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003660; HAMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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IPR000727; TE
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hes 6; Conserv
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Best Local Similarity
                                                                                                             STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                   Mesorhizobium loti
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SEQUENCE 561 AA
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01-MAR-2002
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Q9KKX6;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

MEDLINE=21016719; Pubmed=11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Mhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheak R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.B., Crasay T.H., Dewar K.,

Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hudhes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

Langin-Hooper S., Lee A., Lee J.M., Lauz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Marti R., Marziali A.,

Lin X., Liu S.X., Liu Z.A., Miranda M., Nierman W.C., Osborne B.I.,

Pal G., Peterson J., Palm P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G. Toriumi M.J., Town C.D.,

M. Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

T. Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eddicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                   Gaps
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Pred, No. 61;
1; Mismatches 5; Indels
                                                                                      2; Length 134;
    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 408:816-820(2000).
EMBL, ACO79280, AAGS0577.1; -.
Hypothetical protein.
SEQUENCE 289 AA; 33338 MW; 753AA27BED0F840C CRC64;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ database:
EMBL; AJ231110; CAA13152.1; -.
SEQUENCE 134 AA; 15496 MW; BF340DBC6554BFAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last Sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Hypothetical 33.3 kDa protein.
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                            289 AA
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                                                                                    55.9%; Score 38; DB 63.6%; Pred. No. 28;
                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress)
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MLR3148,
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                                                                                                                                                                        2 FAWORAMRKVR 12
                                                                                                                                                                                                               7 FAWMRALRIKR 17
                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
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Q98GW4;
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RESULT 11 Q98GW4

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3; Indels

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PRELIMINARY;
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RESULT 15
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                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003347; TF_UmjC.
Pfam; PF02373; JmjC; 1...
NON TER 1
SEQÜENCE 1265 AA; 141291 MW; 33DB5BE53A7D9EBE CRC64;
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tive 2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                              Putative zinc finger protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Crordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL, AF21039, AAF63765.1; -
Intertro; IPR003347; FF_JmjC.

Pfam; PF02373; JmjC; 1.

SEQUENCE 1417 AA; 154720 MW; E9CF503D8654FD2B CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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70.0%; Pred. No. 3.1e+02;
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TISSUE=BONE MARROW
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fanson LA, Mattsby-Baltzer I,
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GenCore version 5.1.3.
Copyright (c) 1993 - 2003 Compugen Ltd.
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Dolphin GT;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, collitis, and Candida infections memoral membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food sutfas such as infant formula food. The peptides are also in function have have an also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammatory anti-inflammator
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                        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                           Claim 22; Page 38; 102pp; English.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-linflammatory anti-linfectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative. Gaps ·, New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food Score 54; DB 21; Length 12; Pred. No. 0.0066; 3; Mismatches 0; Indels Dolphin GT Human lactoferrin derived peptide SEQ ID NO:91 Baltzer L, Claim 22; Page 38; 102pp; English. AAY78091 standard; Peptide; 12 AA. Mattsby-Baltzer I, 84.4%; ilarity 75.0%; Conservative 3 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230. 25-APR-2000 (first entry) (ASCI-) A+ SCI INVEST AB. 1 CFQLKKNMKKVR 12 1 CFQLQRNMRKVR 12 WPI; 2000-147388/13. Local Similarity Les 9; Conserv 12 AA; WO200001730-A1. Homo sapiens. Synthetic. 06-JUL-1999; 06-JUL-1998; 17-JUL-1998; 29-DEC-1998; 13-JAN-2000 Hanson LA, Sequence Query Match Best Loca Matches cost. 8888888888888888888888888 Š g 6 AAY78001 to AAY78100 represent peptides having sequences based on human Gaps

New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food

Claim 22; Page 36; 102pp; English.

Dolphin

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food suffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-inflammatory anti-inflammatory be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Pred. No. 0.015;
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98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                     81.2%;
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                                                                                                                                                                                                                                                                                                                                          Conservative
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les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        CFQLKKNMKKVR
                                                                                                                                                                                                                             12 AA;
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                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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ANY8001 to AAY8100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have deaixed anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore provision of peptides based on lactoferrin and costs.
                                                                                                                                                                                                                                                                                                                                          Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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 81.2%; Score 52; DB 21; Length 12; 75.0%; Pred. No. 0.015; 1ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolphin GT
                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:81.
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                                                                                                                                                                                               AAY78081 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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Query Match
Best Local Similarity 75.0
Matches 9; Conservative
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                                                                        1 CFQLKKRWKKVR 12
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                                                                                           1 CFQWKRNWRKVR
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                  AAY78081;
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Gaps

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79.7%; Score 51; DB 21; Length 12; 75.0%; Pred. No. 0.022; ive 2; Mismatches 1; Indels

Conservative

Best Local Similarity Matches 9; Conserv

12 AA;

Sequence Query Match Human, lactoferrin, modification, infection, inflammation, tumou food, infant formula, anti-inflammatory, anti-microbial, anti-tum urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.

Human lactoferrin derived peptide SEQ ID NO:97.

(first entry)

25-APR-2000

AAY78097;

AAY78097 standard; Peptide; 12 AA.

1 CFQLKKNMKKVR

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                       food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                              modification; infection; inflammation; tumour;
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Pred. No. 0.022;
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                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:83.
                                                                                               AAY78083 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 36; 102pp; English.
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75.0%;
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                               (first entry)
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1 CFQWQKNMRKVR 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                   Synthetic.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 19; Page 94; 102pp; English.

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB

98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1.

Homo sapiens. Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through hading to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, and/or prevention of infection on a mucosal curhary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used of infection and may also be used as preservatives. The peptides can also be used and the number of infection and may also be used as preservatives. The peptides can also be used and intitutely on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.1%; Score 50; DB 21; Length 12; 83.3%; Pred. No. 0.033; 2; Indels ive 0; Mismatches 2; Indels
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les 10; Conservative
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Matches
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1; Indels

2; Mismatches

9; Conservative

Matches

RESULT 7 AAY78097

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Gaps

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used as preservatives. In food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired canti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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98SE-0002562.
98SE-0004614.
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29-DEC-1998;
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                               0; Gaps
  Score 49; DB 21; Length 12;
Pred. No. 0.049;
3; Mismatches 1; Indels
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  76.6%;
66.7%;
Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                      1 CFQLKKNMKKVR 12
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||| ::||:|| CFQAQRNMRKVR 12

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RESULT 9 AAY78038

AAY78038 standard; Peptide; 12 AA.

Human lactoferrin derived peptide SEQ ID NO:38. (first entry) 25-APR-2000 AAY78038;

Human; lactoferrin; modification; infection; inflammation; tumour; food; infact formula; anti-inflammatory; anti-microbial; anti-tumou urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

ö AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower Gaps ; 0 Score 48; DB 21; Length 12; Pred. No. 0.073; 3; Mismatches 1; Indels 75.0%; 66.7%; 8; Conservative 1 CFQLKKNMKKVR 12 Query Match Best Local Similarity 12 AA; Sequence Matches ઠે

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 70; 102pp; English.

Dolphin GT

Baltzer L,

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002562. 98SE-0004614.

17-JUL-1998; 29-DEC-1998;

99WO-SE01230.

06-JUL-1999;

13-JAN-2000

WO200001730-A1.

Synthetic.

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RESULT 10

AAY78046 standard; Peptide; 12 AA. AAY78046;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:46.

Human, lactoferrin, modification, infection; inflammation; tumour; food, infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative

sapiens.

WO200001730-A1.

13-JAN-2000

99WO-SE01230 06-JUL-1999;

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Homo sapiens.
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29-DEC-1998;
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Hanson LA,
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                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                   Dolphin GT;
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                                                                                                   Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                     Claim 15; Page 35; 102pp; English
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         98SE-0002441.
98SE-0002562.
98SE-0004614.
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98SE-0002562.
98SE-0004614.
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                                                                     (ASCI-) A+ SCI INVEST AB
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                                                                                                                              WPI; 2000-147388/13.
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         06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
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17-JUL-1998;
29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used to suffect a infammation and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.073;
3; Mismatches 1; Indels
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Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                Claim 18; Page 73; 102pp; English.
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Mattsby-Baltzer I,
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98SE-0004614.
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Matches 8; Conservative
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                                                                   WPI; 2000-147388/13
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane) infections, collitis, and Candida infection on a mucosal membrane) inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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Claim 22; Page 36; 102pp; English
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as

Claim 12; Page 70; 102pp; English.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
             membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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urinary tract infections, colitis, and Candida infection on a mucosal
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                                                                                                                                                                                                                                             75.0%; Score 48; DB 21; Length 13; llarity 66.7%; Pred. No. 0.079; Conservative 3; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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ses 8; Conserv
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17-JUL-1998;
29-DEC-1998;
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Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
uninary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower cost.
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                                                                                                                                                                                         75.0%; Score 48; DB 21; Length 13; 66.7%; Pred. No. 0.079; ive 3; Mismatches 1; Indels
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98SE-0004614.
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Best Local Similarity 66.7
Matches 8; Conservative
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29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000
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                                                                                                                                        Seguence
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AAY78049
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75.0%; Score 48; DB 21; Length 13;

13 AA;

Sequence

Query Match

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              1,
 Pred. No. 0.07
3; Mismatches
                                                                                                Search completed: February 21, 2003, 07:56:45 Job time: 28.093 secs
Best Local Similarity 66.7%; Pr
Matches 8; Conservative 3;
                                      1 CFQLKKNMKKVR 12
                                                   2 CFQWQRNMRKVR 13
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Gaps

0.079;

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NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-08-204-487-3
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39.537 Million cell updates/sec
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                                                                                                                                                                              February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-07-755-161A-3
US-08-204-487-1
US-08-21-24
US-08-21-25-771-25
US-08-21-94-25-
US-08-21-94-25-
US-08-31-94-4-4
US-09-508-734-6
US-09-508-734-6
US-09-508-734-6
US-07-755-161A-10
US-07-755-161A-10
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
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US-07-755-161A-8
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US-07-755-161A-8
US-07-755-161A-8
US-07-755-161A-8
US-08-26-771-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
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Maximum Match 1008
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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64
1 CFQLKKNMKKVR 12
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Maximum DB seq length: 200000000
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Perfect score:
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APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICEAKI
APPLICANT: DOSAKO, SHIN'ICHI
APPLICANT: KAWASAKI, YOSHIMIO
APPLICANT: WINDENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: STREET: S.3 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: COUNTRY: USA
ZIP: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: PAULA A.
REGISTRATION NUMBER: 23.503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENERAL (617) Z48-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENERAL 18 mmino acids
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RESULT 4
US-08-475-055-8
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APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
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                                                   Score 48; DB 1; Length 18; Pred. No. 0.056;
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NEDIUM TYPE: Floppy disk
CMCPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLIANT CATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REPERRORE/DOCKET NUMBER: 947-1-00
TELEPHONE: 201,487-5800
                                                                                                                                                                                                                                         US-08-485-948-8
; Sequence 8, Application US/08485948
; Patent No. 5855882
; GENERAL INFORMATION:
OTHER INFORMATION: (20-37) "
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66.7%;
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
**CANTH: 18 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
MOLECTUE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                     Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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Best Local Similarity
8, Conserv?
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US-08-485-948-8
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US-08-204-487-3
                                                       Query Match
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                                               GENERAL INFORMATION:
APPLICANT: L1, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: CERAM! ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/628,380

FILING DATE: April 4, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION: 314

FILING DATE: APRIL 7, 1995

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 947-1-008 CIP

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION OF 343-1684

TELECOMMUNICATION OF 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 aming acids
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Pred. No. C
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Patent No. 5962245
GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
                                                                                                                                                                                                                                      STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jersey COUNTRY: USA
3, Application US/08628380
5891341
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 66.7
Matches 8; Conservative
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linear
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                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQLKKNMKKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino a
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE: NO
; FRAGMENT TYPE:
US-08-628-380-8
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: 7, note= "thiol group of OTHER INFORMATION: 7, note= "thiol group of OTHER INFORMATION: Cys residue at location 19"
OTHER INFORMATION: thiol group of Cys residue at location 19"
NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: METHOD:
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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-3
                                                                                                                              FILING DATE: 19910905
CLASSIPECATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL INTE:
CELL INTE:
CELL INTE:
CREANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
CLONE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FRATURE:
NAME/KEY: modified site
LOCATION: 2
             OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                       SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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US-07-755-161A-3
US-07-755-161A-3
Sequence 3, Application US/07755161A
Sequence 3, Application US/07755161A
Sequence 3, Application US/07755161A
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
NUMBER OF SEQUENCES:
STREET:
ADDRESSE:
A
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRAY APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.0%; Score 48; Best Local Similarity 66.7%; Pred. No. (Matches 8; Conservative 3; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 06/418,642
FILING DATE: APRLIC 7, 1995
CLASSIFICATION: NUMBER: 06/418,642
FILING DATE: DAPRIC 7, 1995
CLASSIFICATION: 2007
ATVORMEY/ABOUT INFORMATION:
NAME: JACKSON BEG., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELEPHONE: 201 487-5800
TELEPAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUED: 1343-1684
FILEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUED: AMAIO ACID
                                                     STREET: 411 Hackensack Avenue
STREET: Hackensack
STTY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: O7601
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRB PC compatible
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CFOLKKNWKKVR 12
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OTHER INFORMATION: /hote= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"

FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /hote= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
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APPLICANT: NAKASIIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: KAWASAKI, YOSHINRO
APPLICANT: KAWASAKI, YOSHINRO
APPLICANT: WINDENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: S
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 48; DB 1; Length 20; 66.7%; Pred. No. 0.062; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:

ZIP: 02109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
COFRANTING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
TLING DATE: 02-MAR-1994
TLING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATENT ADMINISTRATOR, TESTA, HURWITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                             ) DOCUMENT NUMBER:

FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-204-487-1; Sequence 1, Application US/08204487; Setent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: F. TELECOMMUNICATION INFORMATION TELEFHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: PATENT ADMIN:
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                              DENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CFQWQRNMRKVR 13
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Best Local Similarity
Matches 8; Conserv
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COUNTRY:
                                                                                                                                                                                                                                                                                                                 TITLE:
JOURNAL:
VOLUME:
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                            Gaps
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                            1; Indels
                                                                                                                                                                                                                                                                                   APPLICATION MAINTA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Washington
CITY: Washington
STATE: D.C.
                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.

ZIP: D.C.

ZIP: 2005DINXY: U.S.A.

ZIP: 2005DINXY: U.S.A.

ZIP: 2005DINXY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 50

COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174

FILING DATE: 29-MAY-1992
CLASSIPFCATION: 570

PRIOR APPLICATION STATE:
APPLICATION NUMBER: US 07/755,161

FILING DATE: 05-GRE-1991
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367

REGISTRATION NUMBER: 33,367

REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBENENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEBENENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 5-07-891-174-3
Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 antino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified site
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
                                                                      1 CFQLKKNWKKVR 12
                                                                                               2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
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Gaps
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Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamnor TOMITA et al.
TITLE OF INVENTION:
ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
                                                                                            ;
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| IDENTIFICATION METHOD:
| OTHER INFORMATION: /note= "Cys residues are protected\"to OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
                                         Score 48; DB 1; Length 20;
Pred. No. 0.062;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 20;
Pred. No. 0.062;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF INVENTION: FOLDOLIS INFERTION
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: Diskette, 5.25 inch, 500 kb
COMPUTER: DISKETH: MS-DOS
SOFTWARE: WS-DOS
SOFTWARE: WORDSETECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: UJY 22, 1994
CLASSIFICATION WINBER: US/08/256,771
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, UT.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Best Local Similarity 66.7%;
Matches 8; Conservative
                                              Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                          1 CFQLKKNMKKVR 12
                                                                                                                                                                2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQLKKNMKKVR 12
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US-08-381-984-24
  US-08-256-771-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence (14, Application US/08256771);
Parent No. 568691
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: Wenderoth, Lind & Ponack
CITY: Washington
STREET: 005 Fifteenth Street, N.W., #700
STREET: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                     /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1;
Pred. No. 0.062;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM COMPATIBLE OPERATURG SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: JULY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION: APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
ELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                       NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                 US-08-204-487-1
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US-00-508-734-4

i Sequence 4, Application US/09508734

j Sequence 4, Application US/09508734

j Sequence 4, Application US/09508734

j Patent No. 6423509

j GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Useful microorganism thereof

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT PILING DATE: 1999-00-14

PRIOR PLING DATE: 1999-00-14

PRIOR PLING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                         COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION NUMBER: 325
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: WATEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELESPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48; DB 1;
Pred. No. 0.062;
3; Mismatches
  : 805 Fifteenth Street, N.W., #700 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOLKKNIMKKVR 12
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                                                                             U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                               COUNTRY:
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NAME/KRY:
LOCATION:
LOCATION
DENTIFICATION:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.0%; Score 48; DB 1; Length 20; 66.7%; Pred. No. 0.062; 1; Indels :ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: INM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: APPLICATION APPL:
APPLICATION WIMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER:
TELECOMMUTICATION INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER:
TELECOMMUTICATION INFORMATION:
TELEPAN:
TELENORMATION FOR SEO ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 antho acids
TVPR: amino acids
Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSE; Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-381-984-25
; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENRRAL INFORMATION:
; TITLE OF INVENTION: ANTIOXIDANT
; TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQLKKNMKKVR 12
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2 CFQWQRNMRKVR 13
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Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
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ADDRESSEE: Wenderoth, Lind & Ponack

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/note= "thiol group of
Cys residue at location 21 connected by disulfide bond with
thiol group of Cys residue at location 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cys residue at location 4 connected by disulfide bond with thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 48; DB 1; 66.7%; Pred. No. 0.077; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "thiol group of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
                                   NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAK: 202-371-8856
                                                                                                                                                                            10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION:
LOCATION:
LOCATION:
                                                                                                                                           INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified site
LOCATION: 21
FILING DATE: ITORNEY/AGENT INFORMATION:
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Best Local Similarity 66.7
Matches 8; Conservative
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OTHER INFORMATION: /nc
OTHER INFORMATION: CY
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PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                      ESULT 13
1S-09-508-734-6
1S-09-508-734-6
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENITON: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENITON: useful microorganism thereof
FILE REPRENCE: PASYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
                                                                                             Query Match 75.0%; Score 48; DB 4; Length 22; Best Local Similarity 26.7%; Pred. No. 0.068; Matches 8; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 48; DB 4; Length 24; 66.7%; Pred. No. 0.074;
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15-07-755-161A-10

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

CITY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: U.S.A.
ZIF: 20005
COMPUTER READABLE FORM:
REDIUM TYPE: DISKELEE, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SSCTWARE: KOPAtentin 1.71
LENGTH: 24
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19910905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-6
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
IS-09-508-734-4
                                                                                                                                                                            1 CPOLKKNIMKKVR 12
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
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Pred. No. 0.077;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative 3
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STRAIN:
STRA
                                                                               US-07-81-174-10

Sequence 10. Application US/07891174

Patent No. 5317081

Patent No. 5317081

Patent No. 5317081

Patent No. 5317081

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDERSOR: 10 CORRESPONDENCE ADDERSOR: ADDERSOR: STREET: 80.5 Fifteenth Street, N.W., #700

CITY: Washington Street, S.25 inch, 500KD

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD

COMPUTER: IBM Compatible

COMPUTER: BIM Compatible

COMPUTER: DisplayKrite

COMPUTER: Disp
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NAME/KEY: modified site LOCATION: 21

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Sequence 202, App
Sequence 244, App
Sequence 42127, A
Sequence 2488, App
Sequence 211, Appl
Sequence 33, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 172, Appl
Sequence 1248, Ap
Sequence 1248, Ap
Sequence 1248, Ap
Sequence 1248, Appl
Sequence 36, Appl
Sequence 11530, Appl
Sequence 36, Appl
Sequence 37, Appl
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0 US-09-071-838-202

0 US-09-764-846-244

0 US-09-764-853-738-10

US-09-927-738-11

0 US-09-766-692-2458

US-09-927-107-33

US-09-97-107-33

US-09-97-107-33

US-09-97-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-34

US-09-987-107-38

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-172

US-09-981-875-1728

US-09-981-875-1728
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US-09-866-562-37
                                                                                                                                                                                                                                                   US-09-987-107-35
US-10-155-789-4
US-10-155-789-17
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SYEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILE REPERENCE: A34049-PCT-U3A-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRECESQ for Windows Version 4.0
SEQ ID NO: SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-20
; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
                                                                                                                                                                    9 2 2 2 9 9
     8; Conservative
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1499
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; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQLKKNMKKVR 12
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Best Local Similarity
Matches 8; Conserv
   RESULT 2
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Sequence 52, Appl
Sequence 107, App
Sequence 107, App
Sequence 2, Appli
Sequence 2, Appli
Sequence 2235, Ap
Sequence 2235, Ap
Sequence 2235, Ap
Sequence 2235, Ap
Sequence 2235, Ap
Sequence 2235, Ap
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Sequence 20, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 16, Appli
Sequence 37163, A
                                                                                 February 21, 2003, 08:08:15; Search time 6.88372 Seconds (without alignments) 54.162 Million cell updates/sec
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Compugen Ltd.
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US-09-864-761-37163

US-09-905-9345

US-09-905-9345

US-09-905-933-345

US-09-905-933-345

US-09-841-132-599

US-09-841-132-599

US-09-861-634-00

US-09-861-688-4

US-09-801-138-2335

US-09-801-138-2335

US-09-801-138-2335

US-09-801-138-2335

US-09-801-138-2335

US-09-801-138-2335

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US-10-046-935-2235
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US-09-764-877-1902
US-09-864-761-40172
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US-09-798-869-20
US-10-023-096-2
US-09-798-869-6
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                  156504 segs, 31069816 residues
             GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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64
1 CFQLKKNMKKVR 12
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Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published
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                                                                                                                                                                             Scoring table:
                                                                                                                                            Perfect score:
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                                                                                                                                                                                                                 Searched:
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                                                                                  Run on:
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No.
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Sequence 6, Application US/09798869
Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                          1 CFOLKKNMKKVR 12
                                                                                                                  22 CFOWQRNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFQLKKNMKKVR 12
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US-09-853-625B-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10023096; Patent No. US20020160941A1
| GENERAL INFORMATION:
| APPLICANT: Kruzel, Marian L. APPLICANT: Kruzeki, Tomasz
| APPLICANT: Kurecki, Tomasz
| APPLICANT: Gollnick, Paul D. APPLICANT: Gollnick, Paul D. APPLICANT: Gollnick, Darrell J. ITILE OF INVENTION: Cloning, Expression, and Uses of Human ITILE OF INVENTION: Lactoferrin NUMBER OF SEQUENCES: 8
| CORRESPONDENCE ADDRESS: ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 2004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Jacobson, Price, Holman & Stern
400 Seventh St. N.W.
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7%;
Matches B; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 400 Seventh St
CITY: Washington D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                    TYPE: PRT CORGANISM: Homo Sapiens US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQLKKNWKKVR 12
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; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of Homo sapiens ) OTHER INFORMATION: sequence) US-09-798-869-6
Length 694;
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Pred. No. 0.26;
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Sequence 16, Application US/09853625B
Patent No. US2020049304A1
GENERAL INFORMATION:
TILLE OF INVENTION: Human CCN-Like Growth Factor NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
CRECELL, SYRNE, BAIN, GILFILIAN, CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD
  Score 48; DB 9;
Pred. No. 1.5;
3; Mismatches 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFFWARE: WORD PERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/853,625B
FILING DATE: 14-MAY-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: OFMN SIGURD SVENDSEN

APPLICANT: (YSTEIN REKDAL

APPLICANT: BALDOR SVEINAD (RNSSON

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REPERBNCE: A34049-PCT-USA-A

FILE REPERBNCE: 2001-02-27

PRIOR PLIING DATE: 1999-08-31

PRIOR PLIING DATE: 1999-08-31

PRIOR FLIING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 15
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APPLICATION NUMBER: 09/053,587
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CTHER INFORMATION: EXPRESSED IN LUNG. SIGNAL = 7.2

CTHER INFORMATION: EXPRESSED IN BALIN, SIGNAL = 9.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 10

OTHER INFORMATION: EXPRESSED IN BALIN LIVER, SIGNAL = 7.5

OTHER INFORMATION: EXPRESSED IN BAT74, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BAT74, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BOTE LIVER, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BOTE ANAROW, SIGNAL = 7.7

OTHER INFORMATION: EXPRESSED IN BOTE ANAROW, SIGNAL = 7.7

OTHER INFORMATION: STANDARM HIT: OU7920, EVALUE 1.00e-26

US-09-864-761-37163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.9%; Score 39; DB 10; Length 57; 60.0%; Pred. No. 4.2; 2; Indels tive 2; Mismatches 2; Indels
                   NEGOUR SECTION NO. USCO 1974-879-345

Sequence 345, Application US/09974879

Publication No. US20030028003A1

GENERAL INFORMATION:
TITLE OF INVENTION: 125 Human Secreted Proteins
TITLE OF INVENTION: 125 Human Secreted Proteins
TITLE OF INVENTION: 125 Human Secreted Proteins
TITLE OF INVENTION: 125 Human Secreted Proteins
TITLE OF INVENTION: 125 Human Secreted Proteins
TITLE OF INVENTION: 125 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/974,879
CURRENT FILING DATE: 2000-10-13

PRIOR APPLICATION NUMBER: US 09/305,736

PRIOR FILING DATE: 1999-05-05

PRIOR FILING DATE: 1999-11-04

PRIOR FILING DATE: 1998-11-04

PRIOR FILING DATE: 1998-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,983
PRIOR FILING DATE: 1997-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-11-07
APPLICATION NUMBER: US 60/064,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/064,988
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                       FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPRENCE: Aeomica-X-1
CURRENT PRING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.6%; Score 42; DB 10; Length 351, 66.7%; Pred. No. 7.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                           TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN S-09-853-6258-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIOR PILING DATE: 2000-08-03
RIOR APPLICATION NUMBER: GB 24263.6
RIOR PILING DATE: 2000-10-04
RIOR APPLICATION NUMBER: US 60/236,359
RIOR PILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCI/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIOR FILING DATE: 2000-05-26
RIOR APPLICATION NUMBER: US 09/632,366
RIOR FILING DATE: 2000-05-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 37163, Application US/09864761
Patent No. US20020048763A1
                                                 NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPRONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         LENGTH: 351 AMINO ACIDS TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                             STRANDEDNESS: <Unknown>
                           ATTORNEY/AGENT INFORMATION:
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 CIQTKKSMKAVR 269
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IS-09-864-761-37163
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Gaps

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us-09-743-107b-96.rapb

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Query Match
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                                                                                        251 CYVLSKNMEK 260
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US-10-007-693-107
    US-09-841-132-599
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APPLICANT: Geiger, Benjamin
APPLICANT: Geiger, Benjamin
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Ben-Ze'ev, Avri
APPLICANT: Ben-Ze'ev, Avri
APPLICANTON: BETHODS AND THERAPEUTIC COMPOSITIONS FOR TREATING CANCER
FILE REFERENCE: 01/22326
CURRENT APPLICATION NUMBER: US/09/905,983
CURRENT FILING DATE: 2001-09-28
NUMBER OF SEQ ID NOS: 60
SOFFWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Patent No. US20020061848A1
Fatent No. US20020061848A1
FAPLICANT: Bhatia, Ajay
APPLICANT: Skaky, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND WETHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE FELSE FASTSEQ for Windows Version 3.0/4.0
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Pred. No. 1.1e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               Score 37; DB 9; Length 28; Pred. No. 4.6;
                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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0; Mismatches
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PRIOR APPLICATION NUMBER: US 60/066,100
PRIOR FILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PILING DATE: 1997-11-17
PRIOR PELLING DATE: 1997-11-17
PRIOR PELLING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 611
SSOFWARE: PatentIn Ver. 2.0
SSOFWARE: 28
LENGTH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 52, Application US/09905983 Patent No. US20020045591A1
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-09-905-983-52
                                                                                                                                                                                                                                                                                 CRGANISM: Homo sapiens
JS-09-974-879-345
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QLKKONMKKVR 12
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LENGTH: 784
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LENGTH: 358
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Sequence 43420, Application US/09864761

Facent No. US20020048763A1

GENERAL INFORMATION

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GARE EXPRESSION NALIYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2000-02-04

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-05-26

FRIOR FILING DATE: 2000-06-06

FRIOR FILING DATE: 2000-06-06

FRIOR FILING DATE: 2000-09-07

FRIOR FILING DATE: 2000-09-07

FRIOR FILING DATE: 2000-09-27

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56.2%; Score 36; DB 10; Length 358; 60.0%; Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bratia, Ajay
APPLICANT: Bratia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT APPLICATION NUMBER: 2001-12-05
NUMBER OF SEQ ID NOS: 157
ENGTH: 358
ENGTH: 358
                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis serovar D
US-10-007-693-107
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PRIOR PLICATION NUMBER: PCT/US01/00667
PRIOR PLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                     Sequence 107, Application US/10007693
Patent No. US20020146776A1
GENERAL INFORMATION:
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Gaps
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Stolk, John A.
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITLE OF INVENTION: COMPOSITIONS OF COLON CANCER
FILE REPERENCE: 210121.52761
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT APPLICATION NUMBER: 105/046,935
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 10; Length 347; Pred. No. 1.5e+02; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 371;
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                                                                                                            GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: Giel, Kurt C.
APPLICANT: Giel, Kurt C.
APPLICANT: Wilson, Keith E.
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING COL:
TITLE OF INVENTION: OF SCREENING FOR COLORECTAL CP.
FILE REFERENCE: A-68829-1/DJB/JJD/AMS
CURRENT APPLICATION NUMBER: US/09/851,588
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 09/642,252
PRIOR PELING DATE: 2000-09-17
PRIOR PELING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 347
TYPE: PRT
TYPE: PRT
TYPE: PRT
*** ORGANISM: Homo sapiens
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Patent No. US20020156011A1
GENERAL INFORMATION:
                                                          Sequence 4, Application US/09851588
Patent No. US20020042067A1
GENERAL INFORMATION:
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60.0%;
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Best Local Similarity 60.0
Matches 6; Conservative
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ORGANISM: Homo sapiens
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Matches 6; Conserv
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LENGTH: 371
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Batent No. US2020042385Al

GENERAL INFORMATION:
APPLICANT: Bergsman, Derk S.
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
APPLICANT: Elshourbagy, Nabil
TITLE OF INVENTION: CLONAING OF A NOVEL 7TM RECEPTOR AXOR-2
FILE REFERENCE: GP-70433-C1
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/083,034
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENTH: 373
TYPE: PRT
TYPE: PRT
TYPE: PRT
ORGANISM: HOMO SAPIENS
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Pred. No. 1.1e+02;
2; Mismatches 2; Indels
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Pred. No. 16;
1; Mismatches 3; Indels
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FLING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR FLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 43420
LENGTH: 46
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Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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ORGANISM: Homo sapiens
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US-09-678-178-2235

Sequence 2235, Application US/09878178

Patent No. US200177552A1

GENERAL INFORMATION:

APPLICANT: Jiang, Yuqiu

APPLICANT: Jiang, Yuqiu

APPLICANT: Secrief, Heather

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF COLON CANCER

FILE REPERENCE: 210121.527

CURRENT FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 2237

SOFTWARE FatESQ for Windows Version 4.0

SEQ ID NO 2235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 53.1%; Score 34; DB 9; Length 371; Best Local Similarity 60.0%; Pred. No. 1.6e+02; Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRCANISM: Homo sapiens
FEATURE:
NAME/KEY: variant
CCATION: (1)...(371)
CTHER INFORMATION: Xaa = Any amino acid
US-09-878-178-2235
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Search completed: February 21, 2003, 08:11:58 Job time : 6.88372 secs

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version 5.1.3 - 2003 Compugen Ltd.	<pre>model 48:01 ; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec</pre>	· .	5 roc.dos	esiddes parameters: 283224		ies	·	<pre>g predicted by chance to have a e score of the result being printed, total score distribution.</pre>	SUMMARIES Description	lactotransferi	NOV protein			rna binding protei		secy protein	hypothetical hypothetical	ATP-dependent		secretory pro GLI-related	hypothetic	conserved by conserved by			hypothetical prote cell filamentation	
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ALIGNMENTS

RESULT 1	
TFHUL lactotransferrin precursor [validated] - human	human
N'ALLEIMACE MAMES: IACCOLEITH C;Species: Homo sapiens (man)	
C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #t C;Accession: G01394; S11228; A45401; S10324; S15853;	-Nov-1997 #text change 08-Dec-2000 24; 815853; 820841; 807160; A61169; A31000; 8741
R;Cho, Y. submitted to the EMBL Data Library, March 1994	1994
G06820	
A;Accession: Guis94 A;Status: preliminary; translated from GB/EMBL/DDBJ	/EMBL/DDBJ
A;Molecule type: mRNA A;Regidues: 1-711 <cho></cho>	
3L:U076	236; PIDN: AAB60324.1; PID: 9467237
R; Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pleper, Nucleic Acids Res. 18, 5288, 1990	; Pleper, F.R.
A; Title: Complete nucleotide sequence of human ma	icleotide sequence of human mammary gland lactoferrin.
A; Accession: S11228	
A; Molecule type: mRNA	: :
A;Resiques: 1-148,'T',150-422,'C',424-711 <rby> A:Cross-references: EMBL:X53961: NID:q34415: PIDN</rby>	<pre><rey> 15: PIDN:CAA37914.1; PID:q34416</rey></pre>
R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.	Panella, T.
Mol. Bndocrinol. 6, 1969-1981, 1992	of the estrong action that remilates lactofers
A:Reference number: A45401; MUID:93125571; PMID:1480183	מכנים הישור הישורים
A; Accession: A45401	
A; Molecule type: DNA	
A; Kebidues: 1-13 < 12N3 A; Cross-references: GB: S52659; NID: q263311; PIDN: AAB24877.1;	1; PIDN:AAB24877.1; PID:q263312
A; Experimental source: placenta	
A; Note: sequence extracted from NCBI backbone (NCBIP:122202)	oone (NCBIP:122202)
K;Powell, M.C.; Ogden, C.E. Nicleic Acids Res. 18, 4012, 1990	
A, Title: Nucleotide sequence of human lactoferrin cDNA.	coferrin cDNA.
S10324; N	; PMID:2374734
A;Accession: Sius24	
A,Residues: 3-711 <pow></pow>	
L:X52941; NID:934411; PIDN	11; PIDN:CAA37116.1; PID:934412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, Riochem J 276, 349-355, 1991	rweedie, J.W.
A;Title: Expression of cloned human lactoferrin in baby-hamster	ferrin in baby-hamster kidney cells.
A; Reference number: S15853; MUID:91264786; PMID:2	; PMID:2049066
cid sequence not shown; not	not compared with conceptual translation
A; Resigues: ZU-31 COIL>	
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A; Residues: 20-28,'X',30-31 <st2></st2>	

Length 351;

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Score 42;
Pred. No.
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Best Local Similarity 41.7%;
Matches 5; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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%), Cross-references: GDB:119368; OMIM:150210
%), May position: 321-323
%), May position: 322-323
%), May position: 321-323
%), May position: 321-323
%), May position: 131-326, May position: 4 Exterus predicted < 4516>
%), May position: 131-326, May predicted < 4516>
%), May position: 1310-310 # Exterus predicted < 4516>
%), May position: 1310-310 # Exterus predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May position < 418-356, May predicted < 418-356, May predicted < 418-356, May position < 418-356, May position < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356, May predicted < 418-356
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### Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

### Baction: 200078

### Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000

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### Date: 19-21, 1992

### Date: 10-21, 1992

### Date: 10-20008

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Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: mRNA, A89-711 cRAD>
Residues: 456-487, 47, 489-711 cRAD>
Residues: 456-487, 47, 489-711 cRAD>
Presidues: 456-487, 47, 489-711 cRAD>
Presidues: 456-487, 47, 489-711 cRAD>
Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Panella, T.J.; Liu, X.; Huang, A.T.; Teng, C.T.
Paner Res. 51, 3037-3043, 1991
Thitle: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
Ritle: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
Reference number: A61169; MUID:91235214; PMID:1674448
,Rado, T.A.; Wei, X.; Benz Jr., E.J.
lood 70, 989-993, 1987
;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of
;Reference number: S07160; MUID:88001031; PMID:3477300
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                               Cross-references: EMBL:X59284; NID:g63702; PIDN:CAA41975.1; PID:g63703
Genetics:
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esidues: 'G',23-24,'R', 26-27,'XX',30-32 <HOU>
xperimental source: neutrophil granulocytes
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                                                                                                                                                                                                                                                                                                                             Accession: S07160
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A,Map position: 1
A,Introns: 18/1; 84/2; 125/3; 198/3; 257/3; 337/3; 378/3; 424/3; 477/2; 510/1; 563/3; 63
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A,Residues: 1-223 AMUR-
A);Cross-references: EMBL:Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c
A,Experimental source: strain 972h-; cosmid c19G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
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A;Cross-references: EMBL:U97404; PIDN:AAB93309.1; GSPDB:GN00019; ČESP:ZK770.1
A;Experimental source: strain Bristol N2; clone ZK770
                                                                                                                                                                                                                                                           CiSpecies: Caenorhabditis elegans
CiBate: 29-0ct-1999 #text_change 29-0ct-1999
CiDate: 29-0ct-1999 #sequence_revision 29-0ct-1999 #text_change 29-0ct-1999
CiAccession: T34468
RiMaggi, L.; Gattung, S.; Bartko, L.
submitted to the EMBL Data Library, April 1997
A; Description: The sequence of C. elegans cosmid ZK770.
A; Reference number: Z21530
A; Accession: T34468
A; Status: preliminary; translated from GR/FMRI/Nnb.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Schizosaccharomyces_pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C.Accession: T37974
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Gaps
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A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. ubmitted to the RMBL Data Library, March 1996; Reference number Z21759 Accession: 137974
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Pred. No. 20;
2; Mismatches 1; Indels
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3; Indels
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A,Molecule type: DNA
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Pred. No. 14;
6; Mismatches
   1; Mismatches
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Gaps

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uncharacterized conserved protein CAC2549 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001 C;Accession: A97214

R;Nolling, J.; Breton, G.; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.

Barteriol: 183, 4823-4834, 2007

A;Hitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A;Reference number: A96900; MUID:21359125; PMID:21359225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: DNA
A,Realdues: 1-202 <KIDX
A,Cross-references: GB:AR001437; PIDN:AAK80500.1; PID:g15025572; GSPDB:GN00168
A,Experimental source: Clostridium acetobutylicum ATCC824
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C;Superfamily: Deinococcus radiodurans hypothetical protein DRB0099
                                                                                                                                                                                                                                                                                                                  Query Match
60.9%; Score 39; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels
                      A;Cross-references: BMBL:AL162875
A;Experimental source: cultivar Columbia; BAC clone T32M21
C;Genetics:
                                                                                                                                           A,Map position: 5
A;Introns: 38/3; 78/1; 96/3; 112/3; 145/2; 168/3; 205/3
A;Note: T32M21.200
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Pred. No. 26;
3; Mismatches
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Best Local 'Similarity 58.3%;
Matches 7; Conservative 3
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A;Molecule type: DNA
A;Residues: 1-339 <DOU>
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C; Keywords: nucleomorph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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Alternate names: protein T32M21.200
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Accession: T48456
Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De "es, H.W.; Rude & S.; Lemcke, K.; Mayer, K.F.X.
Demitted to the Protein Sequence Database, March 2000
Reference number: 22448?
                                                                                                                         Accession: T40568
Wood, V.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
ubmitted to the EMBL Data Library, July 1999
Accession: T40568
Accession: T40568
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Sxperimental source: strain Bristol N2; clone F48D6
othetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe) pecies: Schizosaccharomyces pombe ate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Accession: T29242
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Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.
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62.5%; Score 40; DB 2; Length 238;
Best Local Similarity 41.7%; Pred. No. 15;
Matches 5; Conservative 6; Mismatches 1; Indels
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Introns: 46/3; 95/3; 121/3; 173/3; 212/3; 266/2; 302/2
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Dmitted to the EMBL Data Library, May 1996
Description: The sequence of C. elegans cosmid F48D6.
Reference number: 220593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pothetical protein F48D6.2 - Caenorhabditis elegans
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Status: preliminary: translated from GB/EMBL/DDBJ
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155 CYELQQNSKKIK 166
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198 CFLIRKNWKRVK 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQLKKNMKKVR 12
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Molecule type: DNA
Residues: 1-222 <BEV>
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Gene: CESP:F48D6.2
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Gaps

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Length 282; 2; Indels

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C;Species: nucleomorph Guillardia theta
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: D90106
R;Douglas, S; Zauner, S; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit,
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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hypothetical protein orf339 [imported] - Guillardia theta nucleomorph
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Pred. No. 31;
0; Mismatches 2; Indels
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us-09-743-107b-96.rpr

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Length 1553; 0; Indels

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Ajectus: preliminary; not compared with conceptual translation
Ajectus: brilliminary; not compared with conceptual translation
Ajectus: brilliminary; not compared with conceptual translation
Ajectus: brilliminary; not compared with conceptual translation
Ajectus: brillia 4MD.
Ajectus: Fi Ogasawara; N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Enriach, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Ajauthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harvood, C.R.; Hennaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
Ajauthors: Lauber, J.; Lazarevic, V.; Lev, E.; S.; Mosco, M.; Bark, S.H.; Parro, V.; Lapidus, A.; Lardinois,
Ajauthors: Schleich, S.; Rocha, E.; Rocha, B.; Rocha, B.; Sekiguchi, J.; Sekowska, A.; Scanlon,
Ajauthors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Temakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Tamakoshi, A.; Yamanoto, H.; Yamanoto, H.; Yamanoto, K.; Yata, K.; Yata, K.; Yoshida, K.
Ajthors: Yoshikava, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
Ajthors: Yoshikava, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
Ajterence number: A69580; MUID:98044033; PMID:9384377
Ajacension: A69883
Ajacension: A69883
Ajacension: Accusion not shown, translation not shown
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, Residues: 1-1166 (x00>
, Residues: 1-1166 (x00>
, Residues: 1-1166 (x00>
, Ratiosex 1-1166 (x00>
, Halvier Construction (B: Molecular Construction)
, Halvier Construction (B: Molecular Construction)
, Microbiol. 15, 203-211, 1995
, Microbiol. 15, 203-211, 1995
, Title: Expression of the ATP-dependent deoxyribonuclease of Bacillus subtilis is under , Reference number: S61272; MUID: 95264907; PMID: 7746142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Kooistra, J.; Venema, G. Bacteriol. 173, 3644-3655, 1991
| Bacteriol. 173, 3644-3655, 1991
| Fittle: Cloning: sequencing, and expression of Bacillus subtilis genes involved in ATP-3, Reference number: A39432; MUID:91267926; PMID:1646786
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;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Bacillus subtilis
Date: 21-Feb-1992 #sequence revision 21-Feb-1992 #text_change 02-Feb-2001
Accession: A39432; 861272; A69583
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                                                                                                                                                                             2; Mismatches
                                                                                                           Score 39;
Pred. No. 1
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                                                                                                        Query Match 60.9
Best Local Similarity 77.8
Matches 7; Conservative
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hes 7; Conserv
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A;Map position:
A;Note: C0755c
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A;Introns: 51/1;-78/1; 132/2; 161/1; 236/3; 276/3; 295/3; 318/3; 359/3; 397/3; 470/3; 54
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Nolecule type: DNA;
Residues: 1-1162 <WIL>
Cross-references: EMBL:278543; PIDN:CAB01753.1; GSPDB:GN00028; CESP:F29G6.1;
Experimental source: clone F29G6
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:Cross-references: EMBL:Z98551; NID:e1331903; PID:e1331923; PIDN:CAB11141.1
                                                                                                                                                                                                        secY protein - red alga (Cyanidium caldarium)
);Species: Cyanidium caldarium
);Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
Accession: T21557
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Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
Accession: T18502
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-409 < VOG>
A;Residues: 1-409 < VOG>
C;Superfamily: preprotein translocase secY
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60.9%; Score 39; DB 2; Length 409;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 2; Indels

    Caenorhabditis elegans

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                                                                                                                                                                                                                                                                                             C.Accession: S47440
R.Yogel, H.; Valentin, K.
submitted to the EMBL Data Library, August 1994
A.Accession: S47440
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Dimitted to the EMBL Data Library, August 1996

Reference number: Z19441

Accession: T21557
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Jumitted to the EMBL Data Library, August 1997
Reference number: Z18935
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Best Local Similarity 50.0
Matches 6; Conservative
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                       179 FNLKKNKKKV 188
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trons: 10/2; 91/3; 136/1; 159/2; 182/3; 203/1; 225/3; 280/1; 422/3; 466/3; 559/3; 69
722/1; 1779/3; 1843/3; 1908/2; 1941/2; 2007/2
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tle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. ference number: A84420; MUID:20083487; PMID:10617197

atus: preliminary
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idues: 1-2014 <WIL>
jss-references: EMBL:Z78543; PIDN:CAB01757.1; GSPDB:GN00028; CESP:T25C12.3
perimental source: clone F29G6
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ecule type: DNA
idues: 1-2014 <4M13
SS-references: EMBL:Z66566; PIDN:CAA91487.1; GSPDB:GN00028; CESP:T25C12.3
erimental source: clone T25C12
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ss-references: EMBL:293779; PIDN:CAB07849.1; GSPDB:GN00028; CESP:T25C12.3
erimental source: clone H06K08
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                              ecies: Caenorhabditis elegans
te: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change 18-Feb-2000
cession: T21560; T23053; T25270
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02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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tted to the EMBL Data Library, November 1995
erence number: Z20007
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tted to the EMBL Data Library, August 1996
erence number: Z19441
ession: T21560
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Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
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15-UUL-1999 (Rel. 34, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
1-UL-1002 (Rel. 41, Last annotation update)
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MEDLINE=90304039; PubMed=2402455;
REY M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
Nucleic Acids Res. 18:5288-5288(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Mammary gland;
Liang Q., Jimenz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRFL HUMAN STANDARD; PRT; 711 AA.
P02788; Q16780; Q16785; Q16789; Q06726; Q96KZ4;
058684 m 058684 m 058684 m 058684 m 058684 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 05810 m 0
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Wei X., Han J., Rado T.A.;
"Human neutrophil lactoferrin coding and 5' flanking region
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TISSUB-Mammary gland;
TISSUB-Mammary gland;
TISSUB-Mammary gland;
"Cheng H., Chen X., Huan L.;
"CDNA Cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                  VNUC_INBAC
VNUC_INBAD
VNUC_INBP9
                                               YG1B YEAST
SRB3 BRARE
VNUC INBAA
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VNUC_INBESI
D170_HUMAN
HEPA_HSV7J
RPOD_CHLVU
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TISSUE=Mammary gland;
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(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                         CPQLKKNMKKVR 12
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                                                                                                                                                                          February 21,
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Match Length
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181
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aximum DB
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esult No.

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ISSUE=Mammary gland;
                                          resolution.
            Jolles P.;
                   Jolles P.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLINGUED SOURCE J.R., CODIEN G., Han L., Ahmed M.N.,
A CLUMENDED SOURCE J.R., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
A Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
A Gumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
Hejtmancik J.F., Teng C.T.;
Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.;
Mol. Vision 4:31-32(1998).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICABONATE.
-!- FUNCTION: LACTOFERROXIN A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                                                                                                                                  MEDLINE-91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
       Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                             Jameson G.B., Anderson B.F., Vorris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Act Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLUTAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                                                             from human lactoferrin.";
Agric. Biol. Chem. 54:1803-1810(1990).
                                                                          Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF332168; AAG48753.1; -. BC015822; AAH15822.1; -. BC015823; AAH15823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X53961; CAA37914.1; -. EMBL; U07643; AAB60324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M73700; AAA59479.1; -.
X52941; CAA37116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M93150; AAA36159.1; -. M83202; AAA59511.1; -. M83205; AAA58656.1; -. M18642; AAA86665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS THR-30 AND ARG-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA37116.1;
AAB57795.1;
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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
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1LGB; 31-AUG-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9873069;
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PDB;
          McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., MacCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansaria A., Mardis E., Schutz K., Chen C.N., La Basside M., Kaplan N., Greco T., Touchman J., Mazny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Diazanay Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U. Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N., Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-4 resolution."; J. Wol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 609-711.
MEDLINE-82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
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                                                                                                                                                                  SEQUENCE OF 20-711.

MEDLINES B8006667; PubMed-6510420;
MEL2-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
Eur. J. Biochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haridas M., Anderson B.P., Baker B.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An 88 amino acid long C-terminal sequence of human
                                                                  Powell M.J., Ogden J.E.; ""Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 670:243-254(1981).
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MEDLINE=99190892; Pubmed=10089347;
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                                                MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90064528; PubMed=2585506;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actotransferrin.";
EBS Lett. 142:107-110(1982).
SEQUENCE OF 3-711 FROM N.A.
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binding; Signal
                                                                                       NOV PROTEIN. VWFC.
                                                                        POTENTIAL
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                                                                                                                                                                                                                                                          38268 MW;
                                                  Growth factor
                                                                                                                                                                                                                                                                                           65.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002467; UreaseA; 1
PROSITE; PS00145; UREASE 2;
PROSITE; PS01120; UREASE 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D10605; BAA01460.1;
HSSP; P41020; 1UBP.
                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00449; urease; 1
Pfam; PF02802; urease_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactobacillus fermentum
                                                                                                                                                                                                                                                                                                                                                                                                      258 CIOTKKSMKAVR 269
                                                                                                                                                                                                                                                                                                                                                                 1 CFQLKKNWKKVR 12
                                                                                                                                                                                                                                                        351 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; M38.UNW;
                                                        Proto-oncogene;
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                                                                                      CHAIN
DOMAIN
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                             Query Match
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                                                                        SIGNAL
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Provintal rearrangements and overexpression of a new cellular gene (nov) in myeloblastosis-associated virus type 1-induced nephroblastosis-associated virus type 1-induced nephroblastosis-associated virus type 1-induced nephroblastosis-associated virus type 1-induced nephroblastosis-associated virus type 1-induced nephroblastosis.

-i- FUNCTION: IMMEDIATE-EARLY PROTEIN LIKELY TO PLAY A ROLE IN CELL GROWTH REGULATION. ITS OVEREXPRESSION IS ASSOCIATED WITH TUMORIGENESIS AND EXPRESSION OF A N-TERMINAL-TRUNCATED VERSION OF NOV GENE IN CHICKEN BMBRYONIC FIBROBLASTS (CBF) IS SUFFICIENT TO INDUCE THE TRANSPORMATION OF CEF IN VITRO.

-i- TISSUE SPECIFICITY: BRAIN AND HEART, AND AT A LOWER LEVEL IN MUSCLE AND INTESTINE, IN THE EMBRYO, LUNG AND LESS SO IN BRAIN AND SPLEEN, IN ADULT CHICKEN.

-i- DEVELOPMENTAL STAGE: MAVI-INDUCED NEPHROBLASTOWAS EXPRESS A HIGH ADULT KIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN FAMILY. CEF-10/CYREALCTFG/FISP-12/NOV PROTEIN SUBFAMILY. SIMILARITY: CONTAINS 1 WFC DOMAIN. SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
                                                                                                                                                                                                                                                                                                                          NOV.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                    Gaps
                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update).
15-UUN-2002 (Rel. 41, Last annotation update)
NOV protein precursor (Nephroblastoma overexpressed gene protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Brown leghorn;
MEDLINE=92107157; PubMed=1309586;
Joliot V., Martinerie C., Dambrine G., Plassiart G., Brisac M.,
                                                    ;
0
             Score 48; DB 1; Length 711; Pred. No. 0.62;
                                                  1; Indels
                                                                                                                                                                                                                     351 AA
                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; S20078; S20078.
InterPro; IPR00359; Cys knot.
InterPro; IPR00867; INBI_gro_fac_pr.
InterPro; IPR000864; TWP_C.
InterPro; IPR001007; WWP_C.
Pfam; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00222; IGF_BINDING; 1.
             75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X59284; CAA41975.1; -.
         Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SW00041; CT; 1.
SWART; SW00121; IB; 1.
SWART; SW00219; TSP1.
SWART; SW00214; VWC; 1.
PROSITE; PS002222; IGF_B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00219; IGFBP;
                                                                                    1 CFQLKKNMKKVR 12
                                                                                                                       39 CPOWORNMRKVR 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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                                                                                                                                                                                                                 NOV CHICK
P28686;
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SUZUKI K., Takahashi M., Imamura S., Ishikawa T.;
Submitted (XXX.1992) to the EMBL/GenBank/DBU databases.
-!- CATALYTIC ACTIVITY. Urea + H(2)O = CO(2) + 2 NH(3).
-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
-!- SUBUNIT: (ALPHA, BETA, GAMMA)(3) (BY SIMILARITY).
-!- PTM: Lys-22 is carbamylated. The carbamcyl group provides the ligands for the two nickel ions (By similarity).
-!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
                                                                                                                                                                  .) (POTENTIAL)
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L 2 (BY SIMILARITY).
L 1 AND 2 (BY SIMILARITY).
L 1 (BY SIMILARITY).
L 1 (BY SIMILARITY).
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01-AUG-1992 (Rel. 23, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase)
                                                                                                                                                                                                                                                         Score 42; DB 1; Length 351;
BY SIMILARITY.
BY SIMILARITY
BY SIMILARITY
BY SIMILARITY.
BY SIMILARITY.
N-LINEED (GLCNAC. ) (POT)
W, 1ECB3FA3058C6797 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
NCBL_TaxID=1613;
                                                                                                                                                                                                                                                                                    Pred. No. 3.5;
1; Mismatches
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NICKEL
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METAL

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TRFL_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1078; AMINACHANNEL.
TIGRPAMS; TIGR00867; deg-1; 1.
PROSITE; PS01206; ASC; 1.
Hypothetical protein; Ionic channel; Transmembrane; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Magdi L., Gattung S., Bartko L.;
Submitted (AFF-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE AMILORIDE-SENSITIVE SODIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL). (POTENTIAL). (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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Pred. No. 7.4;
2; Mismatches 1; Indels
                                                                          Query Match

65.6%; Score 42; DB 1; Length 573;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 8; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...) (POTEN N-LINKED (GLCNAC...)
                                                                                                                 3; Indels
NICKEL 2 (BY SIMILARITY).
BY SIMILARITY.
; 2D2619781C39E54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90776 MW; 2CAACF7D41770B54 CRC64;
                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Degenerin-like protein ZK770.1 in chromosome
                                                                                                                                                                                                                                                                                           795 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR004726; Deg-1.
InterPro, IPR001873; Na+channel_ASC.
Pfam; PF00858; ASC; 1.
365 NI
325 BY
61805 MW;
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                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                        ZK770.1.
Caenorhabditis elegans.
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365
325
373 AA;
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Best Local Similarity
7; Conserve
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388
458
499
518
795 AA;
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                ACT SITE
SEQUENCE
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TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFRETINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ010930; CAA09407.1; -.
PDB; 1B1X; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
PROSTITE; PS00205; TRANSFERRIN.
PROSTITE; PS00207; TRANSFERRIN. 1; 2.
PROSTITE; PS00207; TRANSFERRIN. 3; 1.
Transport; 1ron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Paramasivam M., Srnitvasan A., Yadav M.P., Singh T.P.,
"CDNA sequence of mare lactoferrin.",
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF AN ANION, USUALLY BICARBONATE.

- SUBUNIT: MONONER.

- SUBCULLUAR LOCATION: Secreted.

- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LACTOTRANSFERRIN
      695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
      STANDARD;
                                                                                                                                                                                                                  Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; 3D-structure.
NON_TER 1
SIGNAL <1
TRFL HORSE
077811;
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                                                                                                                                                                                EMBL, AL096788, CAB46672.1, -.
Hypothetical protein.
SEQUENCE 238 AA, 26479 MW, 58095AA8CD708180 CRC64;
           Nature 415:871-880(2002)
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     SECY_CYACA
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Mood V. Gvilliam R., Rajandeal Babason,
Mood V. Gvilliam R., Rajandeam M., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Comnor R., Cromin A., Davis P., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle B.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., Mclean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblet D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares B., Stewens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whithehead S.,
Welten J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Weltjens I., Vanstreaß E., Raeger M., Schaefer M., Mueller-Auer S.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
Lucas M., Rochet W., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Cerrutti L., Lowe T., McCombie W.R., Peulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                          . . .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                         64.1%; Score 41; DB 1; Length 695; 58.3%; Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                      07BB84D50E1B165D CRC64;
                                                                                                     IRON 1 (BY SIMILARITY).
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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Schizosaccharomyces pombe (Fission yeast).
Bukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
                                                                                                                                                                                                                                                                                   (GLCNAC. . .)
                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC)
N-LINKED (GLCNAC)
N-LINKED (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C582.09 in chromosome II
                                                                                                                                                                                                                                                                                                                                                                                            9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 AA
                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                          75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                             532
601
127
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                                                                                                                                                                                                                                                                                                                                      695 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
Cyanidium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vogel H., Fischer S., Valentin K.-U., "A model for the evolution of the plastid sec apparatus inferred from
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Evol. 51:382-390(2000).
-!- FUNCTION: INVOLVED IN PROTEIN EXPORT. PROBABLY INTERACTS WITH OTHER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE CHLOROPLAST ENDOPLASMIC RETICULUM (CER) MEMBRANES.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast.
-!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gloeckner G., Rosenthal A., Valentin K.-U.; "The structure and gene repertoire of an ancient red algal plastid
                                                                            ö
Score 40; DB 1; Length 238;
Pred. No. 5.5;
6; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                          SECY_CYACA STANDARD; PRT; 410 AA. P46249; QSWD55; 01-NOV-1995 (Rel. 32, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preprotein translocase secY subunit
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TIGREAMS; TIGR00967; 3a05018007; 1.
PROSITE; PS00755; SECY 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secY gene phylogeny.";
Plant Mol. Biol. 32:685-692(1996).
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MEDLINE=20496959; PubMed=11040290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97134960; PubMed=8980520;
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InterPro; IPR002208; SecY.
                                                                     5; Conservative
                                                                                                                                                                         155 CYELQQNSKKIK 166
                                                                                                                                   1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyanidium caldarium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Weiskirchen R., Bister K.;
Submitted (AUG-1994).
Submitted (AUG-1994).
Submitted To the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1994).
GROWIT REGULATION (BY SIMILARITY).
SIMILARITY: BEDONGS TO THE INSCIN'LIKE GROWIT FACTOR BINDING PROTEIN FAMILY.
PROTEIN FAMILY. CEP-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
SIMILARITY: CONTAINS 1 VWFC DOMAIN.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE (CTCK) DOMAIN.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coturnix coturnix japonica (Japanese quail).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOV-1995 (Rel. 32, Last Sequence update)
JUN-2002 (Rel. 41, Last annotation update)
protein precursor (Nephroblastoma overexpressed gene protein)
                                                                                                                                                                                         ;
PROSITE, PS00756; SECY 2; 1.
Protein transport, Transmembrane, Chloroplast, Translocation. CONFLICT 149 149 MISSING (IN REF. 1).
SEQUENCE 410 AA; 46242 MW; 7CB0130175B1DF03 CRC64;
                                                                                                                                   Score 39; DB 1; Length 410;
Pred. No. 13;
                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth factor binding; Signal.
26 POTENTIAL.
353 NOV PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       353 AA.
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U13063; AAA21128.1; -.
InterPro; IPR000359; Cys knot.
InterPro; IPR000867; Insl_gro_fac_pr.
InterPro; IPR000884; TSP1
InterPro; IPR001007; VWF_C.
Fam; PP000007; Cys knot; 1.
Pfam; PF00090; tsp_l; 1.
Pfam; PF00099; vwc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S SWART; SN00121; IB; 1.

SRART; SN00121; IB; 1.

SRART; SM00209; TSP1; 1.

R PROSITE; PS00222; IGF BINDING; 1.

PROSITE; PS01128; CTCK 1; 1.

PROSITE; PS01128; CTCK 2; 1.

PROSITE; PS01208; WPC; 1.

PROSITE; PS01208; WPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
                                                                                                                                   60.9%;
                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                   313 CFELSNNLKK 322
                                                                                                                                                      Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                     1 CFQLKKNWKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=93934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                               NOV COTJA
P42642;
                                                                                                                             Query Match
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NETAINE-98044033; PubMed-9384377; Albertini A.M., Alloni G., KALINE-98044033; PubMed-9384377; Albertini A.M., Alloni G., KALINE-98044033; PubMed-9384377; Albertini A.M., Borchert S., KAZEVEGO V., Bessieres P., Bolotin A., Borchert S., Baretero M.G., Bessieres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S., Borvilse R., Burschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D., And Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D., And Choi S.K., Claser P., Goffeau Y., Fabret C., Ferrari E., Foulger D., And Choi S.K., Glaser P., Goffeau Y., Hajech J., Harwood C.R., Henaut A., Andisepi G., Guy B.J., Haged K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L., Orbasahi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M., Medina N., Meliado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Rarnov, D., Pohl T.M., Portetelle D., Porvollik S., Prescott A., Barto V., Pohl T.M., Portetelle D., Porvollik S., Rose M., Sadale Y., San C., Schola E., Rose M., Sadale Y., Sato T., Scanlan E., Schlaich S., Schroeter R., Scoffone F., Scanlan E., Schlaich S., Schroeter R., Vasumoto K., Yana K., Tacconi B., Taxagi T., Takahashi H., Takemari K., Hambute R., Wanbute R., Wanbute R., Wanbute R., Wanbuter R., Wanbuter R., Wandler E., Wanner E., 
296 333 BY SIMILARITY.
276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
353 AA, 38667 MW, 717D9F8S33882E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kooistra J., Venema G.; "Cloning, sequencing, sopression of Bacillus subtilis genes involved in ATP-dependent nuclease synthesis."; J. Bacteriol. 173:3644-3655 (1991).
                                                                                                                                                                                                                                            ö
                                                                                                                                                     Score 38; DB 1; Length 353;
Pred. No. 17;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus subtilis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168;
Noback M.A., Terpstra P., Holsappel S., Venema G., Bron
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
ATP-dependent nuclease subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=0G1;
MEDLINE=91267926; PubMed=1646786;
                                                                                                            Query Match
Best Local Similarity 58.3.
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                             260 CIRTKKSMKAVR 271
                                                                                                                                                                                                                                                                                                               1 CFQLKKNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicu
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACSU
DISULFID
                                                                          SEQUENCE
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ADDB_BACSU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A39432; A39432.
Subtliist; BG10465; addB.
LinterPro; IPR000512; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding; DNA repair; Complete proteome.

NP BIND 1 22 ATP (POTENTIAL).
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STRAIN=ATCC 27343 / KID;
MEDLINE=560541; PubMed=7476192;
MEDLINE=5605641; PubMed=7476192;
MEDLINE=5605041; PubMed=7476192;
Bork P., Ouzounis C., Casari G., Schneider R., Sander C.,
Dolan M., Gilbert W., Gilbert P.M.;
"Exploring the Mycoplasma capricolum genome: a minimal cell reveals
its Physiology";
Mol. Microbiol. 16:955-967(1995).
-i- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YIGL (B.COLI) / YCSE/YXEH
(B.SUBTILIS) FAMILY.
FUNCTION: THE ENZYME COMPLEX MAY HAVE A WIDE VARIETY OF CATALYTIC ACTIVITIES INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE
                                                                                                                                     SUBUNIT: THE B.SUBTILIS ATP-DEPENDENT NUCLEASE COMPLEX IS FORMED BY ONE B SUBUNIT IN CONJUNCTION WITH ONE A SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1166 AA; 134631 MW; 1A57BBE81A08AB4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Hypothetical protein (Fragment).
Mycoplasma capricolum.
Bacteria, Firmicutes; Mollicutes; Entomoplasmatales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL)
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InterPro; IPR000150; Hypothet_cof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M63489; AAA22200.1; -. EMBL; Y14081; CAA74481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z99109; CAB12902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z33006; CAA83689.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match Best Local Similarity 63.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00702, Hydrolase,
PROSITE, PS01228, COF 1, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESULT 10
125_MYCCA
D _Y125_MYCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIR=ATCS 35210 / B31;
STRAIR=ATCS 35210 / B31;
MEDLINE=98065943; PubMed=9403685;
Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey B.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlawage A.R., Quackenbush J., Salzberg S., Hanson M.,
van Vugt R., Palmer M., Adams M.D., Gocayne J.D., Weldman J.,
Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venter J.C.,
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00471; HDc; 1.
SMRRT; SM00322; KH; 1.
SIGRRAM; TIGROAD; TYPE 1.
PROSITE; PS50084; KH TYPE 1; 1.
Hypothetical protein; Transmembrane; RNA-binding; Complete proteome.
TRANSMEM
                                                                                                                       ö
                                                                                 Score 37; DB 1; Length 267;
Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 510; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                   2; Indels
PROSITE; PS01229; COF_2; 1.
Hypochetical protein.
NON TER 267 267
SEQÜENCE 267 AA; 30425 MW, DS912DD5B39A8451 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58002 MW; A85D675FEA63C668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Borrelia burgdorferi (Lyme disease spirochete).
Bacteria, Spirochaetales, Spirochaetaceae, Borrelia.
(CPL_TaxID=139,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:580-586(1997).
--- SIMILARITY: BELOWGS TO THE UPF0144 FAMILY.
--- SIMILARITY: CONTAINS 1 HD DOMAIN.
--- SIMILARITY: CONTAINS 1 KH DOMAIN.
                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein BB0504.
                                                                                                                                                                                                                                                                       510 AA
                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002819; HD.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH type 1.
InterPro; IPR003607; ME type 1.
Fiam; PF00013; KH-domain; 1.
Fiam; PF00195; HD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE001153; AAC66875.1; -.
                                                                                 57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.8%;
77.8%;
                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                     158 CFGKKENMRQMR 169
                                                                                                                                                 1 CFQLKKNWKKVR 12
                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                   Y504 BORBU
051457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi
                                                                                 Query Match
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                                                                                                   Best Loca
Matches
                                                                                                                                                                                                                                     RESULT 11
Y504_BORBU
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 ô
   Gaps
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

OGUTI T., Katoh O., Takahashi T., Isobe T., Kuramoto K., Hirata S., Yamakido M., Watanabe H.;

"The kruppel-type zinc finger family gene, HKRI, is induced in lung cancer by exposure to platinum drugs.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 314-537 FROM N.A.

MEDLINE=8906896; PubMed=2850480;

Ruppel J. M., Kinzler K.W., Wong A.J., Bigner S.H., Kao F.T.,

Law M.L., Seuanz H.N. O'Brien S.J., Vogelstein B.;

The Gil-Kruppel family of human genes.";

Mol. Cell. Biol. 8:3104-3113 (1988)

-!- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.

-!- SUBCELPULAR LOCATION: Nuclear (Potential).

-!- SIMILABITY: BELONGS TO THE KRUEPPEL FAMILY OF CZHZ-TYPE ZINC-

FINGER PROTEINS.
                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSS0865; KĒĀB; 1.
PROSITE; PSS0152; ZINC_PINGER C2H2_1, 13.
PROSITE; PSS0157; ZINC_FINGER C2H2_2, 13.
Transcription regulation; DNA_bindIng; Zinc-finger; Metal-binding;
                                                                                                                                        HKRL HUMAN STANDARD; PRT; 697 AA.
P10072; Q9UM09;
01-MAR-1989 (Rel. 10, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Krueppel-related zinc finger protein 1 (HKR1 protein) (Fragment).
   ..
 Indels
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0
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PINGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRAB.
ZINC PINGEI
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB013897; BAA86058.1; -.
EMBL; M20675; -; NOT_ANNOTATED_CDS.
PTR; C31201; C31201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001909; KRAB;
Interpro; IPR000822; Znf C2H2.
Pfam; PF00096; zf-C2H2; I3.
Fam; PF01352; KRAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00349; KRAB; 1.
SMART; SM00355; ZnF_C2H2; 13.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:4928; HKR1.
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                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P08047; 1SP2
                                  4 LKKNIMKKVR 12
                                                     |:||:|||
LEKNLKKVR 39
7;
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Paramasivam M., Stinjusaan A., Singh R., Sahani M.S., Singh T.P.;
Paramasivam M., Stinjusaan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO AFONS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBGELLUAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Cameluas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Somall; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.,
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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                                                                                                                                                                                                                                            Score 37; DB 1; Length 697;
Pred. No. 48;
1; Mismatches 3; Indele
                     C2H2-TYPE.
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LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00421; TRANSPERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 2; 2.
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                                                                                                                                                                                                        79552 MW;
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515 CFSLKSNLNK 524
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Best Local Similarity
Matches 6; Conserv
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TISSUE=Brain;
MEDLINE=91283540; PubMed=2059658;
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EMBL; AB035304; BAA87418.1; --
BIRBL; X59796; CAA42468.1; --
PIR, S24306; IJHUCS.
HSSP; P15116; INCJ.
GlycosuiteDB; P33151; --
Genew; HGNC:1764; CDHS.
MIM; 601120;
                                                                                                                                                                                                 iochem. J. 349:159-167(2000).
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                 SEQUENCE FROM N.A.
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=95353875; PubMed=7627717;
Breviario F., Caveda L., Corada M., Martin-Padura I., Navarro Golay J., Introna M., Gulino D., Lampugnani M.G., Dejana E.;
Functional properties of human vascular endothelial cadherin (7B4/cadherin-5), an endothelium-specific cadherin.",
Arterioscler. Thromb. Vasc. Biol. 15:1229-1239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.8%; Score 37; DB 1; Length 708; 58.3%; Pred. No. 49; 3; Indels ive 2; Mismatches 3; Indels
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-> Q (IN REF. 2).
0B0C175A0B69D430 CRC64;
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G -> A (IN REF. 2).
S -> P (IN REF. 2).
LLS -> PLF (IN REF. 2).
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CDH5.
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Best Local Similarity 58.3
Matches 7; Conservative
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708 AA;
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J. Cell Biol. 118:1511-1522(1992).

-I- FUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEINS.

THEY PREPERRATIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS, CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES. THIS CADHERIN MAY PLAY A IMPORTANT ROLE IN RENOTHELIAL CELL BIOLOGY TRROUGH CONTROL OF THE COHESION AND ORGANIZATION OF THE INTERCELLULAR JUNCTIONS. IT ASSOCIATES WITH ALPHA-CAPTENIN FORMING A LINK TO THE CYTOSKELETON.

CHESION AND PROBABLY AT CELL-MATRIX BOUNDARIES.

CHESION SPECIFICITY: RUDOTHELIAL INSUES AND BRAIN.

CHESION SPECIFICITY: RUDOTHELIAL INSUES AND BRAIN.

CHESION SPECIFICITY: CONTAINS 5 CADHERIN DOMAINS.

CHESION SPECIFICATION OFFECD Guide CD144 entry;

WWW="THERETY: CONTAINS 5 CADHERIN GOVALOR" (dd144.htm".)
                                                                                                                                                                                                                                                                                                                                                    PubMod=10861224;
Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
Shimoyama Y., Tsujimoto G., Kitajima M., Natori M.;
"Identification of three human type-II classic cadherins and frequent heterophilic interactions between different subclasses of type-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00028; cadherin, C term; 1.
Pfam; PF01049; Cadherin, C term; 1.
PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA, 5.
PROSITE; PS00202; CADHERIN 1; 3.
PROSITE; PS50268; CADHERIN 2; 5.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suzuki S., Sano K., Tanihara H.;
Dibversity of the cadherin family: evidence for eight new cadherins
in nervous tissue.";
Cell Regul. 2:261-270(1991).
TISSUE=Placenta;
MEDLINE=97362755; PubMed=9219219;
Ali J., Liao F., Martens E., Muller W.A.;
"Vascular endothelial cadherin (VE-cadherin): cloning and role in endothelial cell-cell adhesion.";
endothelial cell-cell adhesion.";
Microcirculation 4:267-277(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Endothelial cells;
MEDLINE-92394977; PubMed=1522121;
Lampupanal M.G., Reanatl M., Raiteri M., Pigott R., Pisacane A., Houen G., Ruco L.P., Dejana E., "A novel endothelial-specific membrane protein is a marker of cell-coll contacts.";
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InterPro; IPR00233; Cadherin_C_term.
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
Nosedale D., Nakahara K., Namath A., Norgpren R., Oeffner P., Oh C.,
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last amocation update)
Hypothetical 31.4 kDa protein in GCN4-WBP1 intergenic region.
VASCULAR ENDOTHELIAL-CADHERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 784;
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                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
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SEQUENCE 282 AA; 31364 MW; 8F7CA122F91E491A CRC64;
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784 AA;
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Search completed: February 21, 2003, 07:51:44 Job time : 7.2093 secs

Q9vzq6 drosophila Q8sqs0 encephalito Q95sh7 drosophila Q6188 caenorhabdi Q919r0 gallus gall Q9bsw9 homo sapien

Q9VZQ6 Q8SQS0 Q95SH7 O61888 Q919R0 Q9ESW9

Q9N003 Q97PW0 Q97TB1

Q98PL7 Q8XJU2

Q98pl7 mycoplasma Q98pl7 mycoplasma Q23447 caenorhadi Q90003 macaca fasc Q97w0 streptococc Q97bb1 streptococc Q97bb1 streptococc Q97bb1 streptococc Q87bb1 plasmodium Q9548 plasmodium Q9876 arabidopsis Q97gr9 neiseria m Q8wp77 plasmodium Q9x76 pascharomyc Q97gr9 neiseria m Q8wp77 plasmodium Q9x76 arabidopsis Q94G5 arabidopsis Q8wp7 plasmodium Q9x719 bacillus an Q8wp7 plasmodium Q97gr1 listeria mo Q97gr1 listeria mo Q97gr1 listeria mo Q97gr1 listeria mo Q97gr1 listeria mo Q91as1 brachydanio

Q8T578 Q95248 Q95248 Q971409 Q95876 Q95876 Q95319 Q80652 Q80652 Q0065376 Q0065376 Q0065376

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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.2%; Score 43; DB 4; Length 711; 63.6%; Pred. No. 27; ive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Straubberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSGF6,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Urease (EC 3.5.1.5) (Urea amidohydrolase).
Lactobacillus fermentum.
                                                                                                                                                                                                                                                                                                                                                    Q8TCD2;
01-UTN-2002 (TrEMBLrel. 21, Created)
01-UTN-2002 (TrEMBLrel. 21, Last seq
01-UTN-2002 (TrEMBLrel. 21, Last ann
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Best Local Similarity 63.00,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=PROSTATE;
                 Lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
0
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Q9S6F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8tcd2 homo sapien
Q9sf6 lactobacill
Q20562 caenorhabdi
Q9ucy5 homo sapien
Q91265 arabidopsis
G9723 clostridium
Q98ck9 homo sapien
Q9hl16 homo sapien
Q9hl16 homo sapien
Q9hl16 homo sapien
Q94116 homo sapien
Q94116 arabidium
Q94436 oryza sativ
Q94365 mus musculu
                                                        February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds (without alignments) 114.078 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
     GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
                                                                                                                                                                  671580 segs, 206047115 residues
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                                         M protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q9S6F6
Q20S6F6
Q20C55
Q9UCY5
Q9TG23
Q9M69
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9BQX9
Q9AVY6
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteria:*
sp_fungi:*
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sp_phage:*
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seq length: 200000000
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Query
Match Length DB
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11553
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325
2014
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Last sequence update)

ALIGNMENTS

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Gaps

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Q9LZ65
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Q9UCY5
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                          Coton E., Visser J.J., Van Vuuren H.J.J.;

L'Acton E., Visser J.J., Van V.J.;

L'Acton E., Van J.J.;

C. -!- CATALYIC ACTIVITY: UREA H. H.(2) 0 = CO(2) + 2 NH(3).

C. -!- CATALYIC ACTIVITY: UREA H. H.(2) 0 = CO(2) + 2 NH(3).

C. -!- CATALYIC ACTIVITY: UREA H. H.(2) 0 = CO(2) + 2 NH(3).

C. -!- SACTOR: EBELONGS TO THE UREASE FAMILY.

EMBL: AT120718; AAD22480.1; -.

R HSSP; P41020; 1UBP.

R PROSITE; P501124; Urease., I.

R PROSITE; P501145; UREASE L; I.

R PROSITE; P501145; UREASE L; I.

R HYDROILS: P501145; UREASE L; I.

R HYDROILS: MARCAL-binding' Nickel.

SEQUENCE 573 AA; 61823 MM; 4D325C6C4A21559C CRC64;
Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales,
Lactobacillaceae, Lactobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.6%; Score 42; DB 2; Length 573;
66.7%; Pred. No. 34;
ive 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BRISTOL N2,
Geisel C., Bradshaw H.;
"The sequence of C. elegans cosmid F48D6.";
Submitted (MAX-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases EMBL, US8732; ABB00596.1; -. Hypotherical protein. SEQUENCE 333 AA; 38150 WW; B2A5ED557CDBA5C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 38.1 kDa protein.
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WEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 66...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             379 CWQLASKMKKVR 390
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                                                                                                            SEQUENCE FROM N.A. STRAIN=TK1214:
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                                                                NCBI_TaxID=1613;
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01-00T-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
Rna binding protein-like (ATSG04600/T32M21_200) (Putative RNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T12M21_200 OR AT5G04600.
Azabidopeis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TAXID=3702;
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Ulang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka I,
Kawai J., Lam B., Lee J.M., Palm C.J., Pham P.K., Quach H.L., Sakurai
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
                                                                                                                                                                                                          Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R.,
De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.
Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.9%; Score 39; DB 4; Length 38; 63.6%; Pred. No. 11; 1. Indels ive 3; Mismatches 1; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR0011156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
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Best Local Similarity 63.6
Matches 7; Conservative
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PRELIMINARY:
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21 FQWQRNMRKVR 31
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HSSP: P02788; 1BKA.
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us-09-743-107b-96.rspt

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Mismatches
                  Pred. No. 60;
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MEDLINE=20087226; PubMed=10618395;
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              58.3%;
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InterPro; IPR000822; Znf_C2H2
Pfam; PF00651; BTB; 1.
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Best Local Similarity 90.0
اتات 8، Conservative
                                   7; Conservative
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                                                                                                          241 CQQLKENISKLR 252
              Best Local Similarity
Matches 7; Conserval
                                                                              1 CFQLKKOWKKVR 12
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Q9AW69
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Yamada K., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,

Lee J.M., Onodera C.S., Quach H.L., Tang C., Torluni M., Wu H.C.,

Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H.,

Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Rawai J., Kim C., Koesema B., Lam B., Lin J., Mayers M.C., Miranda M.,

Narusaka M., Nguyen M., Sakin T., Satou M., Seki M.,

Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Full Length cDNA of gene At5g04600 (GI:15238220).",

Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,

"Full Length cDNA of gene At5g04600 (GI:15238220).",

EMBL, A152875; CAB85566.1;

EMBL, A278899; AAK56702.1;

EMBL, AX05322; AAL36178.1;

InterPro; IPR00076; R.M. rec_mot.

SWART; SM00360; RRW, 1.

PROSITE; PS50102; RRM, 1.

PROSITE; PS50102; RRM, 1.
                                                                                Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayasehizaki Y., Ishhida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M. Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Sato, Shinozaki K., Davis R.W., Tang C.C., Toriumi M., Yamada K., Tu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q., Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I., Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.; "Genome sequence and comparative analysis of the solvent-producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clostridium acetobutylicum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.9%; Score 39; DB 10; Length 222; 100.0%; Pred. No. 49; 0; Mismatches 0; Indels
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"Arabidopsis ORF clones.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                      Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31629 MW; E94EE94D502A5730 CRC64;
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01-00T-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
Uncharacterized conserved protein.
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MEDLINE=21359325; PubMed=11466286;
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Bacteriol. 183:4823-4838(2001).
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Complete proteome.
SEQUENCE 282 AA; 31629 MW
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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80.0%; Pred. No. 70;
.ive 0; Mismatches 2; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL096677; CAC34610.1; -.
HSSP; Q05516; ICS3.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ322G13.2.2 (zinc finger protein FLJ21794, isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 339 AA; 41403 MW; B24EE99E30715629 CRC64;
                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 41.4 kDa protein.
Guillardia theta (Cryptomonas phi).
Bukaryota, Cryptophyta; Cryptomonadaceae; Guillardia.
NCBI_TAXID-55529;
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SMART; SM00225; BTB; 1.
SMART; SM00355; ZNF_C2H2; 5.
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PRELIMINARY;
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Matches
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ID 07
AC 07
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01-MAR-2001 (TrENBLrel. 16, Last sequence update)
01-MAR-2001 (TrENBLrel. 16, Last sequence update)
01-JUN-2002 (TrENBLrel. 21, Last annocation update)
D0322G13.2.3 (zinc finger protein FLJ21794, isoform 3).
D0322G13.2.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, AL096677; CAC17422.1;
HSSP: P07248; 1ARR.
RICEZPRO; IPRO00210; BTB POZ.
RICEZPRO; IPRO00822; Znf_C2H2.
R Pfam; PP000651; BTB. 1.
R Pfam; PP000063; Znf_C2H2; B.
R Probom; PD000003; Znf_C2H2; B.
R SWART; SW00255; BTB; 1.
R SWART; SW00255; BTB; 1.
R SWART; SW00355; Znf_C2H2; 8.
                                                                                                                                    60.9%; Score 39; DB 4; Length 455; 87.5%; Pred. No. 90; ive 0; Mismatches 1; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC FINGER C2H2 1; 4.
PROSITE; PS50157; ZINC FINGER C2H2 2; 5.
DNA-binding; Metal binding; Zinc-finger.
SEQUENCE 455 AA; 51357 MW; 33089B1B7F7CB757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DJ322G13.2.1 (zinc finger protein FLJ21794, isoform 1).
DJ322G13.2.
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PROSITE; PS50097; BTB, 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_1; 7.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 8.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 545 AA; 61982 MW; AAA98208319C361E CRC64;
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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09H117;
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9H116
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1043 CFQL-KNMKQI 1052

01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-UUN-2002 (TrEMBLrel. 21, Last annotation update)

CDC2-related protein kinase. PFC0755C, MAL3P6.10.

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SEQUENCE FROM N.A.

MEDLINE=20087226; PubMed=10618395;
Zauner S., Faunholz M., Wastl J., Penny S.L., Beaton M.,
Zauner S., Faunholz M., Wastl J., Penny S.L., Beaton M.,
Cavaller-Smith T., Maier U., Douglas S.;
"Chloroplast protein and centrosomal genes, a tRNA intron, and odd
telomeres in an unusually compact eukaryotic genome, the cryptomonad
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
|- STMTLARITY: WEAK, TO C.ELEGANS ZK1193.2 AND TO THE C-TERMINAL OF
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Rhabditidae, Peloderinae, Caenorhabditis.
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"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
REL, AJO10592, CAC2708S.1; -.
Hypothetical protein.
SEQUENCE 325 AA; 39399 MW; 27D35E07CD82F083 CRC64;
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                                                                             Q9AV6;
01-JUN-2001 (TERNBLEAL 17, Created)
01-JUN-2001 (TERNBLEAL 17, Last sequence update)
01-JEC-2001 (TERNBLEAL 19, Last annotation update)
Hypothetical 39.4 kba protein.
Guillardia theta (Cryptomonas phi).
Bukaryota, Cryptophyta; Cryptomonadaceae; Guillardia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2014 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21223349; PubMed=11323671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z66566; CAA91487.1; -. Z78543; CAA91487.1; JOINED. Z93779; CAA91487.1; JOINED. Z93779; CAB07849.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAB07849.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CAB01757.1; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOINED
                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 CVLIKKNIKKI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQLKKNWKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleomorph.
                                               Q9AVY6
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Q22774
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                                                                                                                                                                                                                                        Bowman S., Lawson D., Basham D., Brown D., Chillingworth T., Churcher C.W., Craig A., Davies R.M., Devlin K., Feltwell T., Gentles S., Gwilliam R., Hamiln N., Harris D., Holroyd S., Hornsby T., Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S., Mungall K., Murphy D., Oliver K., Quail M.A., Rajandream M.-A., Whitehead S., Skelton J., Squares R., Squares S., Stanton J.E., Whitehead S., Woodward J.K., Newbold C., Barrell B.G., "The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; I. Prodom; P000001; Euk pkinase; I. Prodom; P0000001; Euk pkinase; 2. Prodom; P0000001; Euk pkinase; 2. PROSITE; PS00107; PROTEIN KINASE ATP; 1. PROSITE; PS00108; PROTEIN KINASE DOM; 1. PROSITE; PS00108; PROTEIN KINASE ST; 1. ATP-binding; Kinase; Serine/Chreonine-protein kinase; Transferase. 1553 AA; 182218 MW; E23D3C3416F1E8EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            904E36 PRELIMINARY; PRT; 1167 AA.
094E36,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
05-JUN-2002 (TrEMBLrel. 21, Last annotation update)
05-JUN-20032H19.19 protein.
07-yza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhattoldeae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 falciparum .";

Nuture 400:532-538(1999).

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; Z98551; CAB11441.1; -.

InterPro; IPR000719; Buk_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sabaki T., Matsumoto T., Yamamoto K.;
Noryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC clone:OSNBB0032H19.";
Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.9%; Score 39; DB 5; Length 1553; 77.8%; Pred. No. 2.5e+02; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone:OSJNBb0032Hi9.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AP003219; BAB61186.1;
InterPro; IRR03653; SUMO protease.
Pfam; PF02902; Peptidase C48; 1.
SEQUENCE 1167 AA; 131408 MW; 6308AB28A292CIF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.2%; Score 38.5; DB 10; 72.7%; Pred. No. 2.4e+02; ive 2; Mismatches 0;
                                                                                                                                                                                                          MEDLINE=99376085; PubMed=10448855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duery Match
Sest Local Similarity 72.7
(atches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                           SEQUENCE FROM N.A.
                                                              NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | | | | | | 39 MKKONMKKVK 47
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Query Match

SULT 13

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Gaps

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Indels

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InterPro; IPR001561; EGF-like.
InterPro; IPR001364; Lectin_C.
InterPro; IPR001364; Lectin_C.
InterPro; IPR001364; Lectin_C.
InterPro; IPR001364; Lectin_C;
SMART; SW00131; CGF-1;
SWART; SW00131; EGF; 3.
SWART; SW001327; VWA; 1.
PR05ITE; PS00022; EGF-1; UNKNOWN-S.
PR05ITE; PS01186; EGF-1; UNKNOWN-S.
PR05ITE; PS01345; VWFA; 1.
Hypothetical protein.
SEQUENCE 2014 AA; 221261 WW; 65E3BC76440C73BB CRC64;
COMERY MATCH.
SEQUENCE 2015 SF: SCORE 38; DB 5; Length 2016
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Hearch completed: February 21, 2003, 08:00:50 ob time: 23.6744 secs